?d s1/3/1-12

Medline 6/17-93

Display 1/3/1

08504054 93214054
Mobilization of hematopoietic stem and progenitor cell subpopulations from the marrow to the blood of mice following cyclophosphamide and/or granulocyte colony-stimulating factor.
Neben S; Marcus K; Mauch P
Joint Center for Radiation Therapy, Harvard Medical School, Boston, MA 02115.
Blood (UNITED STATES) Apr 1 1993, 81 (7) p1960-7, ISSN 0006-4971 Journal Code: A8G
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/2

08453069 93163069
Peripheral blood stem cell mobilization by cytokines.
Ahmed T; Wuest D; Ciavarella D
New York Medical College, Valhalla 10595.
J Clin Apheresis (UNITED STATES) 1992, 7 (3) p129-31, ISSN 0733-2459 Journal Code: HID
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

- end of record -

?

Display 1/3/3

08392390 93102390
Peripheral blood stem cell mobilization after stem cell factor or G-CSF treatment: rapid enrichment for stem and progenitor cells using the CEPRATE immunoaffinity separation system.
Heimfeld S; Fogarty B; McGuire K; Williams S; Berenson RJ
CellPro, Incorporated, Bothell, Washington 98021.
Transplant Proc (UNITED STATES) Dec 1992, 24 (6) p2818, ISSN 0041-1345 Journal Code: WE9
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/4

08095168 92233168
[The role of stem cell mobilization in the scope of autologous blood stem cell transplantation]
Die Rolle der Stammzell-Mobilisation im Rahmen der Autologen Blutstammzell-Transplantation (ABSZT).
Korbling M
M. D. Anderson Cancer Center, University of Texas, Houston.
Beitr Infusionther 1991, 28 p233-41, ISSN 1011-6974 Journal Code: BZI
Languages: GERMAN Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL English Abstract

- end of record -

?

Display 1/3/5

07865980 92003980

Transplantation with blood stem cells.
Zander AR; Lyding J; Bielack S
Department of Hematology-Oncology, Universitatskrankenhaus Eppendorf, Hamburg, FRG.
Blood Cells 1991, 17 (2) p301-9, ISSN 0340-4684 Journal Code: A8H
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

- end of record -

?
Display 1/3/6

07765556 91284556
Mobilization of haemopoietic stem cells by cyclophosphamide into the peripheral blood of patients with haematological malignancies.
Shepherd KM; Charles P; Sage RE; Dale BM; Norman JE; Kotasek D; Gregg A; Futter J
Department Haematology/Oncology, Queen Elizabeth Hospital, Woodville, Australia.
Clin Lab Haematol 1991, 13 (1) p25-32, ISSN 0141-9854 Journal Code: DKF
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?
Display 1/3/7

07408512 90315512
The median daily increment of leukocytes during hematopoietic recovery reflects the myeloid progenitor cell yield during leukapheresis in children.
Emminger W; Emminger-Schmidmeier W; Hocker P; Gerhartl C; Kundi M; Gadner H
St. Anna Children's Hospital, Vienna, Austria.
Bone Marrow Transplant Jun 1990, 5 (6) p419-24, ISSN 0268-3369 Journal Code: BON
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?
Display 1/3/8

07292259 90199259
Therapeutic efficacy of autologous blood stem cell transplantation (ABSCT): the role of cytotoxic/cytokine stem cell mobilization.
Korbling M; Haas R; Knauf W; Holle R; Hunstein W
Institut f. Medizinische Biometrie, Heidelberg University, FRG.
Bone Marrow Transplant Jan 1990, 5 Suppl 1 p39-40, ISSN 0268-3369 Journal Code: BON
Languages: ENGLISH
Document type: CLINICAL TRIAL; JOURNAL ARTICLE

- end of record -

?
Display 1/3/9

06054168 87028168
Complement split product C5a mediates the lipopolysaccharide-induced mobilization of CFU-s and haemopoietic progenitor cells, but not the mobilization induced by proteolytic enzymes.
Molendijk WJ; van Oudenaren A; van Dijk H; Daha MR; Benner R
Cell Tissue Kinet Jul 1986, 19 (4) p407-17, ISSN 0008-8730 Journal Code: CQA
Languages: ENGLISH

Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/10

04259195 81087195
Pyran copolymer: effect of molecular weight on stem cell mobilization in mice.
Zander AR; Spitzer G; Verma DS; Ginzbarg S; Dicke KA
Biomedicine May 1980, 33 (3) p69-72, ISSN 0300-0893 Journal Code: A5P
Contract/Grant No.: CA-24770; CA-23077
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/11

03321676 77223676
Mobilization of B and T lymphocytes and haemopoietic stem cells by polymethacrylic acid and dextran sulphate.
van der Ham AC; Benner R; Vos O
Cell Tissue Kinet Jul 1977, 10 (4) p387-97, ISSN 0008-8730 Journal Code: CQA
Languages: ENGLISH
Document type: JOURNAL ARTICLE

- end of record -

?

Display 1/3/12

02860675 76041675
Polymethacrylic acid: induction of lymphocytosis and tissue distribution.
Ross WM; Martens AC; van Bekkum DW
Cell Tissue Kinet Sep 1975, 8 (5) p467-77, ISSN 0008-8730 Journal Code: CQA
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Set	Items	Description
S1	12	STEM(W)CELL(W)(MOBILIZ? OR PERIPHERALIZ?)
S2	22	VERY(W)LATE(W)ANTIGEN(W)4
S3	0	S2 AND STEM(W)CELL
S4	183	VASCULAR(W)CELL(W)ADHESION(W)MOLECULE
S5	1	S4 AND STEM(W)CELL

?

Display 5/3/1

08217769 92355769
Role of beta 1 and beta 2 integrins in the adhesion of human CD34hi stem cells to bone marrow stroma.
Teixido J; Hemler ME; Greenberger JS; Anklesaria P
Department of Tumor Virology, Dana Farber Cancer Institute, Boston, Massachusetts 02115.
J Clin Invest Aug 1992, 90 (2) p358-67, ISSN 0021-9738 Journal Code: HS7
Contract/Grant No.: CA-39851; DE-08798; CA42368
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Display 1/3/3 (Item 3 from file: 5)

B10815

WPI

9805466 BIOSIS Number: 44055466
PERIPHERAL BLOOD STEM CELL MOBILIZATION AFTER STEM CELL FACTOR OR G-CSF TREATMENT RAPID ENRICHMENT FOR STEM AND PROGENITOR CELLS USING THE CEPRATE IMMUNOAFFINITY SEPARATION SYSTEM
HEIMFELD S; FOGARTY B; MCGUIRE K; WILLIAMS S; BERENSON R J
CELLPRO INC., 22322 20TH AVE. SE, SUITE 100, BOTHELL, WASH. 98021.
FIRST INTERNATIONAL CONGRESS OF THE CELL TRANSPLANT SOCIETY, PITTSBURGH, PENNSYLVANIA, USA, MAY 31-JUNE 3, 1992. TRANSPLANT PROC 24 (6). 1992. 2818. CODEN: TRPPA
Language: ENGLISH
Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/5 (Item 5 from file: 5)

9769786 BIOSIS Number: 44019786
COMPARISON OF PERIPHERAL BLOOD STEM CELL MOBILIZATION BY THREE REGIMENS
JANSSEN W E; ELFENBEIN G J; LEE C; SMILEE R; CARTER R; PACH M; LEPARC G F ; SINALDI E; MASSARO P; ET AL
H. LEE MOFFITT CANCER CENT., UNIV. SOUTH FLA. COLL. MED., TAMPA, FLA.
45TH ANNUAL MEETING OF THE AMERICAN ASSOCIATION OF BLOOD BANKS, SAN FRANCISCO, CALIFORNIA, USA, NOVEMBER 7-12, 1992. TRANSFUSION (ARLINGT) 32 (8 SUPPL.). 1992. 43S. CODEN: TRANA
Language: ENGLISH
Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/6 (Item 6 from file: 5)

9347558 BIOSIS Number: 43092558
PERIPHERAL BLOOD STEM CELL MOBILIZATION AFTER STEM CELL FACTOR SCF ON G-CSF TREATMENT RAPID ENRICHMENT FOR STEM AND PROGENITOR CELLS USING THE CEPRATE IMMUNOAFFINITY SEPARATION SYSTEM
HEIMFELD S; ANDREWS R; ZSEBO K; FOGARTY B; MCGUIRE K; WILLIAMS S; BERENSON R
CELLPRO INC., BOTHELL, WASH.
XXI ANNUAL MEETING OF THE INTERNATIONAL SOCIETY FOR EXPERIMENTAL HEMATOLOGY, PROVIDENCE, RHODE ISLAND, USA, JULY 26-30, 1992. EXP HEMATOL (N Y) 20 (6). 1992. 748. CODEN: EXHMA
Language: ENGLISH
Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/7 (Item 7 from file: 5)

8884735 BIOSIS Number: 42109735
PERIPHERAL BLOOD STEM CELL MOBILIZATION RAPID ENRICHMENT OF PROGENITOR CELLS USING A UNIQUE BIOTIN-AVIDIN IMMUNOAFFINITY SEPARATION SYSTEM
HEIMFELD S; BENSINGER W; FOGARTY B; MCGUIRE K; WILLIAMS S; ZSEBO K; BERENSON R
CELLPRO INC., BOTHELL, WASH. 98021.
KEYSTONE SYMPOSIUM ON HEMATOPOIESIS, TAMARRON, COLORADO, USA, FEBRUARY 27-MARCH 5, 1992. J CELL BIOCHEM SUPPL 0 (16 PART C). 1992. 65. CODEN: JCBSD
Language: ENGLISH
Document Type: CONFERENCE PAPER

- end of record -

?

Display 1/3/8 (Item 8 from file: 5)

8871887 BIOSIS Number: 42096887
PERIPHERAL BLOOD STEM CELL MOBILIZATION RAPID ENRICHMENT OF PROGENITOR

CELLS USING A UNIQUE BIOTIN AVIDIN IMMUNOAFFINITY SEPARATION SYSTEM
  BERENSON R; ANDREWS R; BENSINGER W; FOGARTY B; MCGUIRE K; WILLIAMS S; HEIMFELD S
  CELLPRO INC., BOTHELL, WASHINGTON 98021, USA.
  KEYSTONE SYMPOSIUM ON BONE MARROW TRANSPLANTATION, KEYSTONE, COLORADO, USA, JANUARY 19-26, 1992. J CELL BIOCHEM SUPPL 0 (16 PART A). 1992. 189.
CODEN: JCBSD
  Language: ENGLISH
  Document Type: CONFERENCE PAPER

- end of record -

?
      Display 1/3/12   (Item 12 from file: 5)

7329393   BIOSIS Number: 38109914
  THERAPEUTIC EFFICACY OF AUTOLOGOUS BLOOD STEM CELL TRANSPLANTATION ABSCT THE ROLE OF CYTOTOXIC-CYTOKINE STEM CELL MOBILIZATION
  KOERBLING M; HAAS R; KNAUF W; HOLLE R; HUNSTEIN W
  MED. KLINIK POLIKLINIK V, INST. F. MED. BIOMETRIC, HEIDELBERG UNIV., FRG.
  INTERNATIONAL SYMPOSIUM ON PERIPHERAL BLOOD STEM CELL AUTOGRAFTS, MULHOUSE, FRANCE, OCTOBER 15-17, 1989. BONE MARROW TRANSPLANT 5 (SUPPL. 1). 1990. 39-40. CODEN: BMTRE
  Language: ENGLISH
  Document Type: CONFERENCE PAPER

- end of record -

?
      Display 1/3/13   (Item 13 from file: 5)

7329385   BIOSIS Number: 38109906
  APPROACHES TO BLOOD STEM CELL MOBILIZATION INITIAL AUSTRALIAN CLINICAL RESULTS
  JUTTNER C A; TO L B; HAYLOCK D N; DYSON P G; BRADSTOCK K F; DALE B M; ENNO A; SAGE R E; SZER J; TOOGOOD I R G
  LEUKAEMIA RES. UNIT, IMVS, FROME RD., ADELAIDE, SOUTH AUSTRALIA, AUST. 5000.
  INTERNATIONAL SYMPOSIUM ON PERIPHERAL BLOOD STEM CELL AUTOGRAFTS, MULHOUSE, FRANCE, OCTOBER 15-17, 1989. BONE MARROW TRANSPLANT 5 (SUPPL. 1). 1990. 22-24. CODEN: BMTRE
  Language: ENGLISH
  Document Type: CONFERENCE PAPER

- end of record -

?
      Display 1/3/16   (Item 16 from file: 5)

2965749   BIOSIS Number: 69003156
  THE MECHANISM OF HEMOPOIETIC STEM CELL MOBILIZATION A ROLE OF THE COMPLEMENT SYSTEM
  WILSCHUT I J C; ERKENS-VERSLUIS M E; PLOEMACHER R E; BENNER R; VOS O
  DEP. CELL BIOL. GENET., ERASMUS UNIV., P.O. BOX 1738, ROTTERDAM, NETH.
  CELL TISSUE KINET 12 (3). 1979. 299-312. CODEN: CTKIA
  Full Journal Title: Cell and Tissue Kinetics
  Language: ENGLISH

- end of display -

?ds

Set	Items	Description
S1	19	STEM(W)CELL(W)(MOBILIZ? OR PERIPHERALIZ?)
S2	38	VERY(W)LATE(W)ANTIGEN(W)4
S3	0	S2 AND STEM(W)CELL
S4	252	VASCULAR(W)CELL(W)ADHESION(W)MOLECULE
S5	0	S4 AND STEM(W)CELL
S6	0	S1 AND S2
S7	0	S1 AND S4

? Display 9/3/15 (Item 15 from file: 5)

7754915 BIOSIS Number: 90122915
VASCULAR CELL ADHESION MOLECULE-1 MEDIATES LYMPHOCYTE ADHERENCE TO CYTOKINE-ACTIVATED CULTURED HUMAN ENDOTHELIAL CELLS
CARLOS T M; SCHWARTZ B R; KOVACH N L; YEE E; ROSSO M; OSBORN L; CHI-ROSSO G; NEWMAN B; LOBB R; HARLAN J M
DIV. HEMATOL., ZA-34, HARBORVIEW MED. CENT., 325 9TH AVE., SEATTLE, WASH. 98104.
BLOOD 76 (5). 1990. 965-970. CODEN: BLOOA
Full Journal Title: Blood
Language: ENGLISH

APS

```
L6            5 L1 AND L4 AND L5

=> d 1-5

1.  5,188,959, Feb. 23, 1993, Extracellular matrix protein adherent T
cells; Allan B. Haberman, 435/240.243, 4, 240.2 [IMAGE AVAILABLE]

2.  5,187,193, Feb. 16, 1993, Method for stimulating transplanted bone
marrow cells; Richard F. Borch, et al., 514/476 [IMAGE AVAILABLE]

3.  5,169,765, Dec. 8, 1992, Method for stimulating production of bone
marrow cell growth factors using dithiocarbamates; Richard F. Borch, et
al., 435/70.4, 69.5, 69.52 [IMAGE AVAILABLE]

4.  4,965,195, Oct. 23, 1990, Interleukin-7; Anthony E. Namen, et al.,
435/69.52, 91, 172.1, 172.3, 320.1; 530/350, 351; 536/24.3, 24.31 [IMAGE
AVAILABLE]

5.  4,808,402, Feb. 28, 1989, Method and compositions for modulating
neovascularization; Samuel J. Leibovich, et al., 424/78.06, 423, 618;
514/2 [IMAGE AVAILABLE]

=>
  (FILE 'USPAT' ENTERED AT 11:27:00 ON 17 JUN 93)
L1         58124 S BLOOD
L2             0 S STEM(W)CELL#(W)(MOBILIZ? OR PERIPHERALIZ?)
L3             0 S STEM(W)CELL#(W)(MOBILIZ?)
L4           145 S STEM(W)CELL
L5           154 S CYTOKINE
L6             5 S L1 AND L4 AND L5

=>
d 18 1-3

1.  5,188,959, Feb. 23, 1993, Extracellular matrix protein adherent T
cells; Allan B. Haberman, 435/240.243, 4, 240.2 [IMAGE AVAILABLE]

2.  4,965,195, Oct. 23, 1990, Interleukin-7; Anthony E. Namen, et al.,
435/69.52, 91, 172.1, 172.3, 320.1; 530/350, 351; 536/24.3, 24.31 [IMAGE
AVAILABLE]

3.  4,808,402, Feb. 28, 1989, Method and compositions for modulating
neovascularization; Samuel J. Leibovich, et al., 424/78.06, 423, 618;
514/2 [IMAGE AVAILABLE]

=>
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Teng, S
977702
seqs 1 & 2

Seq. 1

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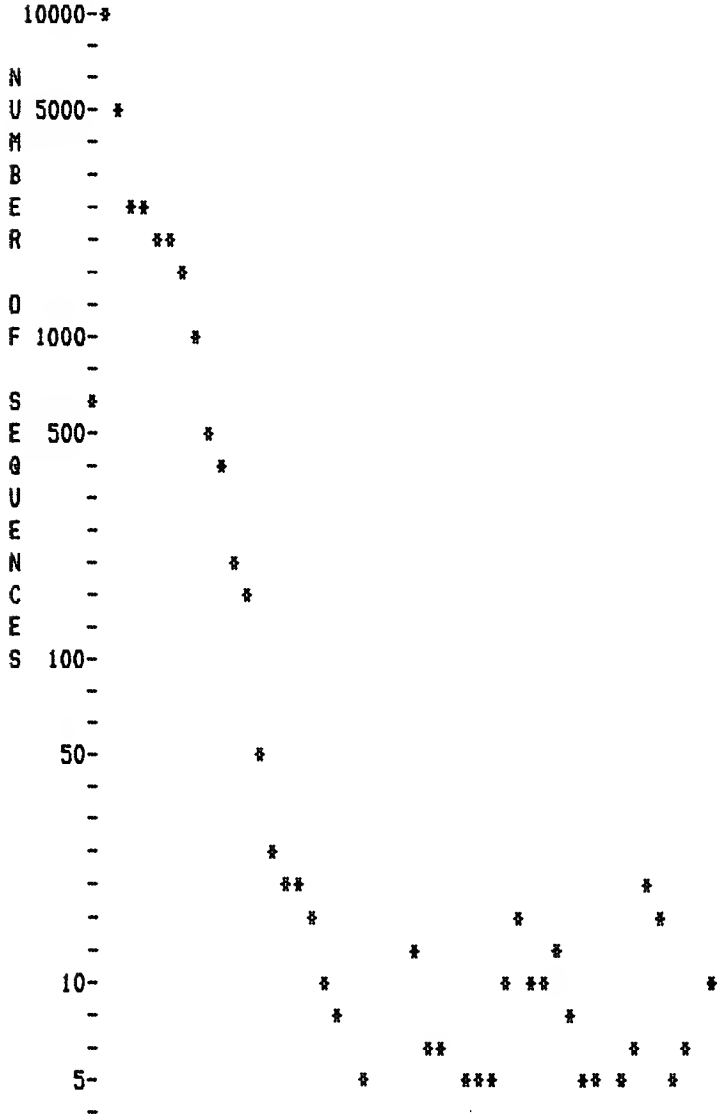
> 0 <
0| |0  IntelliGenetics
> 0 <

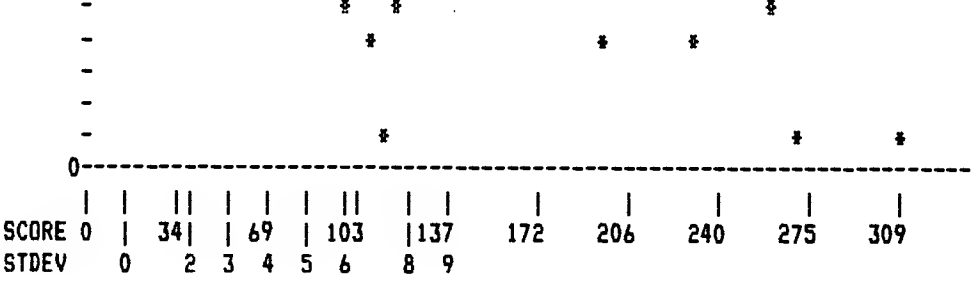
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-977-702-1-ngs.res made by shears on Tue 15 Jun 93 11:23:42-PDT.


Query sequence being compared:US-07-977-702-1 (1-360)
Number of sequences searched:              25646
Number of scores above cutoff:              4455

     Results of the initial comparison of US-07-977-702-1 (1-360) with:
   Data bank : N-GeneSeq 10, all entries
```





PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	32
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		
Initial scores to save	40	Alignments to save	15
Optimized scores to save	0	Display context	50

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	17	14	13.65

Times:	CPU	Total Elapsed
	00:03:12.02	00:06:39.00

Number of residues: 14371384
Number of sequences searched: 25646
Number of scores above cutoff: 4455

Cut-off raised to 9.
Cut-off raised to 15.
Cut-off raised to 22.
Cut-off raised to 28.
Cut-off raised to 32.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 21 standard deviations above mean ****					
1. Q11098	Encodes gamma heavy chain of	861	309	316	21.40	0
	**** 18 standard deviations above mean ****					
2. Q10381	Chimeric MAb 9.2.27 heavy cha	363	270	279	18.54	0
	**** 17 standard deviations above mean ****					
3. Q08607	Co-1 Heavy Chain V Region (mo	471	259	265	17.73	0
4. Q22736	RSV19 VH.	348	256	299	17.51	0
5. Q28739	cDNA of VH425 antibody cloned	501	256	269	17.51	0
	**** 16 standard deviations above mean ****					
6. Q23863	ScFvB18 construct mutant #6.	770	236	280	16.05	0
7. Q23862	ScFvB18 construct mutant #5.	770	236	280	16.05	0
8. Q23861	ScFvB18 construct mutant #4.	770	236	280	16.05	0
9. Q23860	ScFvB18 construct mutant #3.	770	236	280	16.05	0
10. Q23859	ScFvB18 construct mutant #2.	770	236	280	16.05	0

11.	Q21100	ScFvB18 construct.	770	236	280	16.05	0
		**** 15 standard deviations above mean ****					
12.	Q23858	ScFvB18 construct mutant #1.	770	234	279	15.90	0
13.	Q15164	VH186 region of anti-nitrophe	458	233	277	15.83	0
14.	Q06227	VH domain of antibody C again	345	229	245	15.53	0
15.	N91482	Genomic to cDNA junction (V47	349	228	269	15.46	0
16.	Q12013	Sequence encoding mouse MAb 2	477	226	259	15.31	0
17.	Q12057	Sequence encoding heavy chain	477	226	259	15.31	0
18.	Q27141	ICAM-1 inhibiting peptide 2.	387	225	263	15.24	0
19.	Q06957	Genomic sequence encoding hea	2675	225	260	15.24	0
20.	N91820	DNA sequence of the V and J r	443	224	262	15.17	0
21.	Q28263	Fv(FRP51)-ETA fusion gene.	2012	223	270	15.09	0
22.	Q28260	FWP51 fusion gene.	748	222	269	15.02	0
23.	Q12637	Monoclonal antibody OK3T heav	1570	222	268	15.02	0
		**** 14 standard deviations above mean ****					
24.	Q28258	FWP51 heavy chain variable do	342	218	259	14.73	0
25.	N91146	2H7 Vh sequence.	458	218	266	14.73	0
26.	N70968	Sequence of the anti-hepatiti	420	217	264	14.65	0
27.	N70967	Sequence of the anti-hepatiti	420	217	264	14.65	0
28.	Q04261	Encodes Colon Cancer monoclon	456	217	239	14.65	0
29.	N70971	2H7 VH sequence which contain	459	217	265	14.65	0
30.	Q23342	Murine heavy chain variable r	354	216	261	14.58	0
31.	N91645	Heavy chain of monoclonal ant	540	216	270	14.58	0
32.	Q04040	Anti-Leu 3a heavy chain varia	765	216	262	14.58	0
33.	Q04262	Encodes Colon Cancer monoclon	416	215	239	14.51	0
34.	Q08609	ME4 Heavy Chain V Region (mou	492	215	261	14.51	0
35.	Q04463	Heavy chain variable region o	361	214	238	14.43	0
36.	Q04258	Sequence homologous to TAG72	982	214	252	14.43	0
37.	Q28522	Hypercalcaemia agent cDNA por	356	213	251	14.36	0
38.	Q24790	Anti-Tac antibody heavy chain	433	213	247	14.36	0
39.	Q05600	Anti-Tac heavy chain variable	433	213	247	14.36	0
40.	Q05554	Sequence encoding variable re	446	213	233	14.36	0

1. US-07-977-702-1 (1-360)
   Q11098 Encodes gamma heavy chain of T84.66 monoclonal ant

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 ID   Q11098 standard; DNA; 861 BP.
 AC   Q11098;
 DT   08-MAY-1991  (first entry)
 DE   Encodes gamma heavy chain of T84.66 monoclonal antibody.
 KW   MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
 KW   human adenocarcinoma; mouse-human chimaeric antibody; ss.
 OS   Mus musculus.
 FH   Key             Location/Qualifiers
 FT   exon            272..317
 FT   /*tag=  a
 FT   intron          318..395
 FT   /*tag=  b
 FT   exon            396..770
 FT   /*tag=  c
 FT   promoter        109..118
 FT   /*tag=  d
 FT   /note= "putative"
 FT   promoter        121..127
 FT   /*tag=  e
 FT   /note= "putative"
 FT   promoter        160..166
 FT   /*tag=  f
 FT   /note= "putative"
 FT   promoter        169..176
 FT   /*tag=  g
 FT   /note= "putative"
 PN   WO9101990-A.
 PD   21-FEB-1991.
 PF   19-JUL-1990; U04049.
```

PA (CITY) CITY OF HOPE.
PI Shively JE, Riggs AD, Neumaier M;
DR WPI; 91-073486/10.
DR P-PSDB; R11384.
PT Novel anti-CEA antibody - comparable to ATCC Accession No. BH
PT 8747, produced by recombinant DNA, used in diagnosis of tumours
PS Claim 4; Page 18; 24pp; English.
CC The heavy chain variable region of murine MAb 84.66 was cloned and
CC sequenced as follows: Hybridoma DNA was extracted, completely
CC restricted with EcoRI and run on a gel. Fragments were extracted and
CC ligated in the EcoRI site of Lambda-ZAP.Phage were packaged and plated.
CC Plaque screening was with a 991bp XbaI fragment from the mouse
CC enhancer region, a 1.5kb cDNA fragment from the heavy chain
CC constant region gene of hybridoma CEA.66-E3 and a 5.4kb EcoRI
CC fragment containing an aberrantly rearranged heavy chain from
CC Sp2/0. Positive clones were further characterised by hybridisation
CC to J-region oligonucleotides (see Q10842-Q10846) and sequenced. The
CC murine gamma variable region gene was used to produce mouse V-human C
CC antibodies with high affinity for CEA. Chimaeric murine-human anti-
CC CEA Abs are used to diagnose human colon adenocarcinomas.
CC See also Q10834-Q10841 and Q10847-8.
SQ Sequence 861 BP; 213 A; 208 C; 203 G; 237 T;

Initial Score = 309 Optimized Score = 316 Significance = 21.40
Residue Identity = 88% Matches = 322 Mismatches = 33
Gaps = 10 Conservative Substitutions = 0

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                                                X       10        20
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                                                ||  | ||||||||||||||||
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 360       370       380       390       400       410       420       430

        30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGAGCTTGTGGAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
         440       450       460       470       480       490       500

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAATGGATTGGAAGGATTGATCCTGCGAATGGTA
       510       520       530       540       550       560       570

    170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
   ||| |||||||| |||||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
   ATAGTAAATATGTCCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
     580       590       600       610       620       630       640

  240       250       260       270       280       290       300
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACG-
   ||||||||| |||||||||||||||||||||||||||||| || |||||   ||   | ||| || | |||
   TGCAGCTCACCAGCCTGACATCTGAGGACACTGCCGTCTATTATTGTGC-TCCG---TTTGGTTA-CTACGT
   650       660       670       680       690       700           710

     310       320       330       340       350       X
   ----GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
       |  |||||| ||| || |||||| ||||| ||| | ||||||||||||||||
   GTCTGACTATGCTATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGGTAAGAATGGCCTCTC
      720       730       740       750       760       770       780

   CAGGTCTTTATTTTTAACCTTTGTATGGACTTT
    790       800       810
```

2. US-07-977-702-1 (1-360)
Q10381 Chimeric MAb 9.2.27 heavy chain variable region DN

ID Q10381 standard; DNA; 363 BP.
AC Q10381;
DT 15-APR-1991 (first entry)
DE Chimeric MAb 9.2.27 heavy chain variable region DNA sequence.
KW Chimeric antibodies; human glycoprotein antigen; melanoma; cancer;
KW ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..363
FT /*tag= a
FT /product= H-chain V-region of MAb 9.2.27
PN EP-411893-A.
PD 06-FEB-1991.
PF 31-JUL-1990; 308402.
PR 31-JUL-1989; US-387665.
PA (ELIL) ELI LILLY & CO.
PI Beavers LS, Bumol TF, Gadski RA;
DR WPI; 91-038771/06.
DR P-PSDB; R10541.
PT Monoclonal antibody contg. recombinant DNA - binds to human
PT chondroitin sulphate proteoglycan on melanoma cells for melanoma
PT treatment and diagnosis
PS Claim 11; page 18; 33pp; English.
CC This sequence, contained in vector pG4G21, is ligated to a DNA
CC sequence encoding a human heavy (H) chain constant (C) region, in
CC the construction of pN9.2.27G1. This vector is used to transform
CC host cells, in conjunction with vector pG9.2.27K contg. murine
CC light (L) chain variable (V) region and human L- chain C- region.
CC The resulting host cell expresses the chimeric antibody 9.2.27
CC which is directed against proteoglycans of human melanoma cells.
CC This chimeric monoclonal antibody (MAb) is useful in the diagnosis
CC and treatment of melanoma. The use of human C-regions avoids the
CC problems associated with murine monoclonals e.g. rapid clearance
CC from the bloodstream due to anti-self recognition.
CC See also Q10379-81 and Q10382-84.
SQ Sequence 363 BP; 88 A; 87 C; 105 G; 83 T;

Initial Score = 270 Optimized Score = 279 Significance = 18.54
Residue Identity = 78% Matches = 285 Mismatches = 72
Gaps = 6 Conservative Substitutions = 0

```
      X       10        20        30        40        50        60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||| | ||||||||||||||  | ||||| |||||||| |||||||||| ||| | ||||||| ||||
   CAGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAAGCT
      X    10        20        30        40        50        60        70

  70        80        90       100       110       120       130       140
   TCTGGCTTCAACATTAAAGA-CACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGAT
   ||||||| |  |||| |  |   | |  ||| ||||||||||||||||||||| |||||| || ||||||||
   TCTGGCTAC-GCATTCAGTAGGTCTTGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGAT
         80        90       100       110       120       130       140

         150       160       170       180       190       200       210
   TGGAAGGATTGATCCTGCGAG-TGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAG
   |||| ||||| |||||| ||| ||| |||||||| ||  |   ||||||| ||| |||||||||  | || |
   TGGACGGATTTATCCTG-GAGATGGAGATACTAACTACAATGGGAAGTTCAAGGGCAAGGCCACACTGACTG
      150       160       170       180       190       200       210

         220       230       240       250       260       270       280
   CGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACT
```

```
CAGACAAATCCTCCAGCACAGCCTACATGCAGGTCAGCAGCCTGACCTCTGTGGACTCTGCGGTCTATTTCT
   220       230       240       250       260       270       280

     290       300       310       320       330       340       350
GTGC-AGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTC
|||| ||| |||||   ||||  |      ||| || |||||| |||||| ||||| ||| | |||||||||
GTGCAAGAGGGAAT-ACGGTAGTAGTTCCCTATACTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC
 290       300       310       320       330       340       350

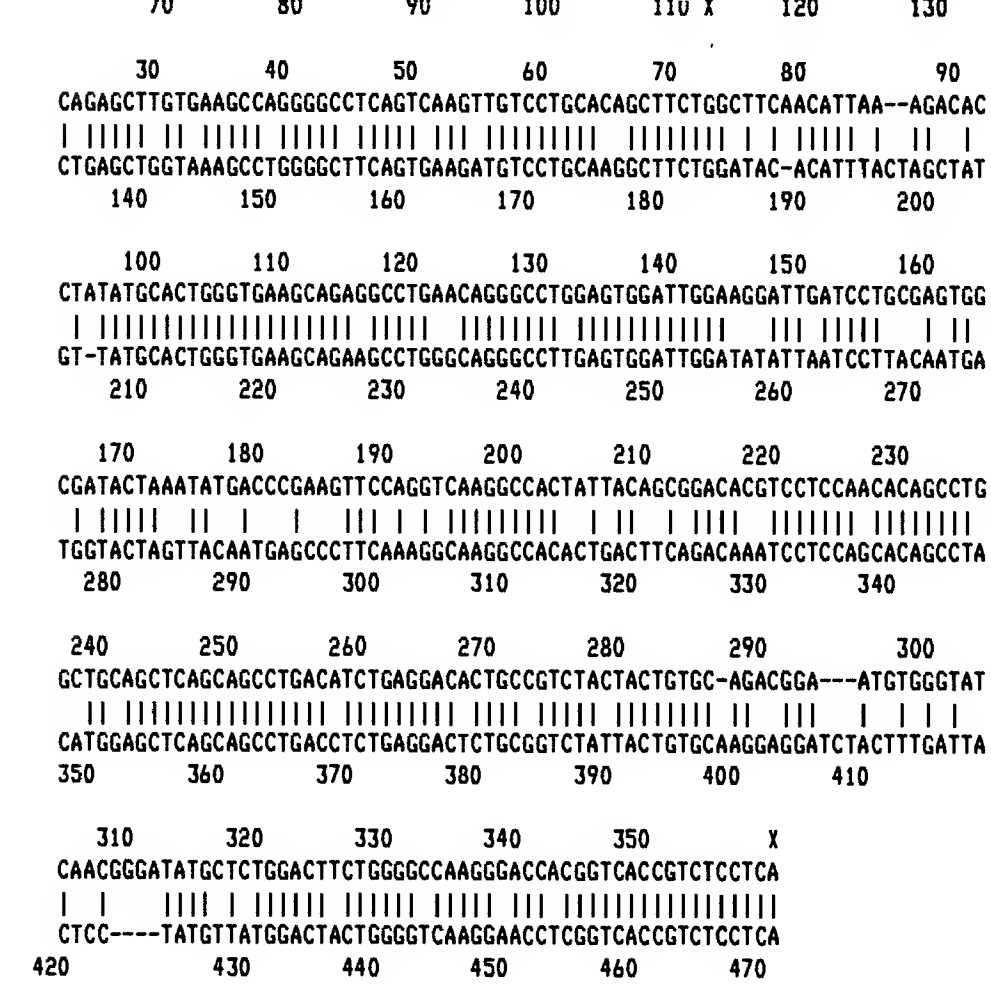
   360
TCCTCA
||||||
TCCTCA
360  X
```

3. US-07-977-702-1 (1-360)
   Q08607 Co-1 Heavy Chain V Region (mouse).

```
 ID   Q08607 standard; DNA; 471 BP.
 AC   Q08607;
 DT   04-MAR-1993  (first entry)
 DE   Co-1 Heavy Chain V Region (mouse).
 KW   Monoclonal antibody; chimera; light; heavy; chain; constant;
 KW   variable; antigen; diagnosis; cancer; tumour; ss.
 OS   Mus musculus.
 FH   Key             Location/Qualifiers
 FT   CDS             52..471
 FT   /*tag=  a
 PN   WO9002569-A.
 PD   22-MAR-1990.
 PF   06-SEP-1989; U03852.
 PR   06-SEP-1988; US-240624.
 PR   08-SEP-1988; US-241744.
 PR   13-SEP-1988; US-243739.
 PR   04-OCT-1988; US-253002.
 PR   19-JUN-1989; US-367641.
 PR   21-JUL-1989; US-382768.
 PA   (ITGE-) INT GENETIC ENG INC.
 PI   Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
 DR   WPI; 90-115825/15.
 DR   P-PSDB; R09425.
 PT   Chimeric mouse-human antibodies - prepd. using genes coding for
 PT   constant human region  murine variable region, esp. to 3 tumour
 PT   antigen
 PS   Claim 13; Page 123 + Fig 22; 173pp; English.
 CC   Shown is the nucleotide sequence from the end of the oligo-dC tail
 CC   to the Jh4-Ch1 junction.  The sequence is used in the prodn. of a
 CC   chimeric antibody mol. comprising two light chains and two heavy chains,
 CC   each having a constant region (human) and a variable region (murine)
 CC   having specificity to an antigen bound by murine monoclonal antibody
 CC   (MAb) Co-1.  The chimeric antibodies can be used for any purpose for
 CC   which the original murine MAbs can be used, with the advantage that
 CC   they are more compatible with the human body.  They are esp. used for
 CC   the diagnosis and treatment of cancer.
 SQ   Sequence   471 BP;    115 A;    120 C;    115 G;    121 T;

Initial Score    =    259  Optimized Score  =    265  Significance = 17.73
Residue Identity =    74%  Matches          =    273  Mismatches   =    81
Gaps             =     12  Conservative Substitutions              =     0

                                                X       10        20
                                                GTCAAACTGCAGCAGTCTGGGG
                                                ||| | ||||||||||||||||
   GTTGGATATTTCTCTTTCTCCTGTCAGGAACTGCAGGTGTCCACTCTGAGGTCCAGCTGCAGCAGTCTGGAC
```



4. US-07-977-702-1 (1-360)
   Q22736 RSV19 VH.

ID Q22736 standard; DNA; 348 BP.
AC Q22736;
DT 13-AUG-1992 (first entry)
DE RSV19 VH.
KW VH; VK; donor; antibody; CDR; epitope; NEW; REI;
KW fusion protein; F protein; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT misc_feature 91..105
FT /*tag= a
FT /label= CDR1
FT misc_feature 149..199
FT /*tag= b
FT /label= CDR2
FT misc_feature 296..316
FT /*tag= c
FT /label= CDR3
FT primer_bind 2..23
FT /*tag= d
FT /note= "corresponds to primer sequence used"
FT primer_bind 316..349
FT /*tag= e
FT /note= "corresponds to primer sequence used"
PN WO9204381-A.
PD 19-MAR-1992.
PF 11-SEP-1991; G01554.
PR 11-SEP-1990; GB-019812.
PA (SCOT-) SCOTGEN LTD.
PI Harris WJ, Tempest PR, Taylor G;
DR WPI; 92-114306/14.

DR P-PSDB; R24807.
PT New altered antibodies with donor MAb binding specificity for RSV
PT - for treatment and prevention of human respiratory syncytial
PT virus infection
PS Disclosure; Fig 1; 72pp; English.
CC The sequences of RSV19 VH and VK are represented in Q22736 and Q22737
CC respectively. The donor antibody RSV19 is directed against epitope
CC 417-438 of the fusion protein (F). The CDRs were identified (see
CC features), then the murine CDRs transferred to human frameworks by
CC site-directed mutagenesis, using as DNA templates human framework
CC regions of the NEW (heavy) and REI (light) proteins.
CC The altered antibodies are used to prevent or treat RSV infections
CC in humans, e.g. for prevention they are given (each 6 weeks during
CC the RSV season) at 1-20 mg/kg parenterally or 0.2-2 mg/kg
CC intranasally. Since the antibodies are predominantly
CC human, they are unlikely to cause much immune response.
SQ Sequence 348 BP; 84 A; 91 C; 95 G; 76 T;
SQ 2 Others;

Initial Score = 256 Optimized Score = 299 Significance = 17.51
Residue Identity = 84% Matches = 305 Mismatches = 40
Gaps = 15 Conservative Substitutions = 0

```
      X       10        20        30        40        50        60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||| | ||||||||||||||||| ||||||||| || | ||||||||||||||||||||||||||||||||
   CAGGTCCAGCTGCAGSAGTCWGGGACAGAGCTTGAGAGGTCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      X    10        20        30        40        50        60        70

  70        80        90       100       110       120       130       140
   TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
   ||||||||||||||||||||  |||||||||||||| |||||||||||||||| ||||||||||||||||||
   TCTGGCTTCAACATTAAAGACTACTATATGCACTGGATGAAGCAGAGGCCTGACCAGGGCCTGGAGTGGATT
         80        90       100       110       120       130       140

       150       160       170       180       190       200       210
   GGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCG
   ||| ||||||||||||  || ||  |||  | |||||| ||||||||||||||| |||||||||||  || ||
   GGATGGATTGATCCTGAGAATGATGATGTTCAATATGCCCCGAAGTTCCAGGGCAAGGCCACTATGACTGCA
      150       160       170       180       190       200       210

      220       230       240       250       260       270       280
   GACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGT
   ||||||||||||||||||||||  |||||||||| |||||||||| |||||||||||||||||  | ||||
   GACACGTCCTCCAACACAGCCTACCTGCAGCTCACCAGCCTGACATTTGAGGACACTGCCGTCTATTTCTGT
    220       230       240       250       260       270       280

     290       300       310       320       330       340       350
   GCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCC
          |||       |||  |||   ||   | |||  ||||||||||||||||||||||||||||||||
   --------AAT-------TCATGGGGGAGTGACTTTGACCACTGGGGCCAAGGGACCACGGTCACCGTCTCC
          290              300       310       320       330       340

   360
   TCA
   |||
   TCA
     X
```

5. US-07-977-702-1 (1-360)
Q28739 cDNA of VH425 antibody cloned into pUC18.

ID Q28739 standard; DNA; 501 BP.
AC Q28739;
DT 01-MAR-1993 (first entry)

DE CDNA of VH425 antibody cloned into pUC18.
KW Monoclonal antibody; complementarity determining region; framework;
KW antigens; tumour; melanoma; carcinoma; glioma; variable; heavy;
KW light; chain; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 30..450
FT /*tag= a
FT sig_peptide 30..87
FT /*tag= b
FT mat_peptide 88..450
FT /*tag= c
FT primer_bind 10..32
FT /*tag= d
FT /note= "3'-5' PCR primer binding site"
FT primer_bind 12..32
FT /*tag= e
FT /note= "PCR primer binding site"
FT primer_bind 436..465
FT /*tag= f
FT /note= "3'-5' PCR primer binding site"
PN WO9215683-A.
PD 17-SEP-1992.
PF 04-MAR-1992; E00480.
PR 06-MAR-1991; EP-103389.
PA (MERE) MERCK PATENT GMBH.
PI Bendig MM, Kettleborough CA, Saldanha J;
DR WPI; 92-331729/40.
DR P-PSBD; R27049.
PT Human monoclonal antibodies binding to human receptors - for
PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma
PS Disclosure; Fig 2; 89pp; English.
CC The cDNA sequence encoding the variable heavy chain of monoclonal
CC antibody 425 was prepd. synthetically and mutations made to the 5'
CC and 3' ends to allow for cloning into HCMV expression vectors.
CC Donor splice sites were recreated in the 3' flanking regions to
CC allow correct splicing of the variable and constant regions. The
CC 5' sequence was altered to introduce an initiation codon. These
CC mutations were carried out using the PCR primers shown in the
CC features table. The cloned chimeric antibody contg. 425 VL and
CC 425 VH regions were cotransfected into COS cells to confirm cloning
CC of the correct mouse base variable sequence. The cloned antibody
CC may be used int the prodn.of reshaped or humanised antibodies which
CC are less immunogenic than native antibodies and may be used to combat
CC e.g. glioma, melanoma or carcinoma.
CC See also Q27040-1.
SQ Sequence 501 BP; 127 A; 146 C; 124 G; 104 T;

Initial Score = 256 Optimized Score = 269 Significance = 17.51
Residue Identity = 75% Matches = 275 Mismatches = 82
Gaps = 6 Conservative Substitutions = 0

```
                                                X       10        20
                                                GTCAAACTGCAGCAGTCTGGGG
                                                ||| | ||||| ||  ||||||
    GCTATATCATCCTCTTTTTGGTAGCAACAGCTACAGATGTCCACTCCCAGGTCCAGCTGCAACAACCTGGGG
           50        60        70        80        90       100       110

         30        40        50        60        70        80        90
    CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTA-AAGACACC
    | || || |||||||| ||||| ||||| |||||||||||||  ||||| |||| || | | |  || || |
    CTGAACTGGTGAAGCCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCCGGCTACACCTTCACCAGCCA-C
         120       130       140       150       160       170       180

       100       110       120       130       140       150       160
    TATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGC
```

```
TGGATGCACTGGGTGAAGCAGAGGGCTGGACAAGGCCTTGAGTGGATCGGAGAGTTTAATCCCAGCAACGGC
    190       200       210       220       230       240       250

  170       180       190       200       210       220       230
GATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGG
  |||||| ||  |   ||| ||| ||  |||||||||  | || |  ||||  ||||||| ||||||||
CGTACTAACTACAATGAGAAATTCAAGAGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC
  260       270       280       290       300       310       320

240       250       260       270       280       290       300
CTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTG-CAGAC-GGAATGTGGGTATCAA
 |||| |||||||||||||||||||||| |||| ||||| ||||||| ||| | ||| | ||  || | |
ATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCCAGTCGGGACTATGATTA-CGA
330       340       350       360       370       380       390

310       320       330       340       350         X
CGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
|||    | || | |||| |||||||||||| |||||  |||| |||||||||
CGGACGGTACT-TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACACCCCATC
400       410       420       430       440       450       460

  GGTCTATCCACTGGATTCCTCTAGAGTCGAC
470       480       490       500
```

6. US-07-977-702-1 (1-360)
   Q23863 ScFvB18 construct mutant #6.

```
ID   Q23863 standard; DNA; 770 BP.
AC   Q23863;
DT   21-MAY-1992  (first entry)
DE   ScFvB18 construct mutant #6.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1..770
FT   /*tag=  a
FT   /product= scFvB18
FT   mutation        734
FT   /*tag=  b
FT   /note= "c -> t; Thr -> Ile (VL FR4)"
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
DR   P-PSDB; R22587.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 38; Fig 44; 209pp; English.
CC   The sequence encodes an antibody scFv fragment directed against 4-
CC   hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC   against NP were separately amplified and reassembled to form the
```

CC construct, which was then ligated into the f8 gene III contg. vec-
CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
CC into fdDOGKan (fdCAT2 with the tet gene replaced by a kanamycin
CC resistance gene) to give fdDOGKanscFvB18, or into the phagemid
CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
CC the effect of using mutator strains to increase the diversity of
CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
CC After 4 rounds of mutation and screening, 40 phage inserts were
CC sequenced. They each displayed single mutations in 6 different
CC positions, five being in the light chain region. More than 70% of
CC the mutations occurred at positions 724 and 725 changing the first
CC Gly in the J segment (framework 4) to Ser (in 21 cases here) or
CC Asp (in 3 cases). The mutant shown here (see feature table for
CC details of the mutation) occurred once. The mutant fragments had
CC affinities for NP which were comparable to the wild-type scFv
CC fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
CC 736-738, and 793-862.
SQ Sequence 770 BP; 188 A; 196 C; 214 G; 172 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
Residue Identity = 79% Matches = 288 Mismatches = 65
Gaps = 11 Conservative Substitutions = 0

```
                    X       10        20        30        40        50
                    GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                    ||| | ||||||||||||||||| ||||||||||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
        10        20 X      30        40        50        60        70

       60        70        80        90       100       110       120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| |||||||||  |||||||||| || | | |    | ||  |||||||||||||||||||||||| |
AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
      80        90       100       110       120       130       140

    130       140       150       160       170       180       190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
|  ||||| |||||||||||||||||||||||   ||||| | |||||| ||  |  |||||||| ||  |
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
   150       160       170       180       190       200       210

  200       210       220       230       240       250       260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||||  | || |  ||||   ||||||  ||||||||   ||||||||||||||||||||||||||||
AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
 220       230       240       250       260       270       280

270       280       290       300       310       320       330
ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
 ||||  |||||  || |||||  |||   || |  ||  ||| | ||    ||  || | ||||  |||||||||
TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
290       300       310       320       330               340       350

  340       350         X
AGGGACCACGGTCACCGTCTCCTCA
|||||||||||||||||||||||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
   360       370       380       390       400       410       420

GGC
```

7. US-07-977-702-1 (1-360)
   Q23862 ScFvB18 construct mutant #5.

ID Q23862 standard; DNA; 770 BP.
AC Q23862;
DT 21-MAY-1992 (first entry)
DE ScFvB18 construct mutant #5.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..770
FT /*tag= a
FT /product= scFvB18
FT mutation 725
FT /*tag= b
FT /note= "g -> a; Gly -> Asp (VL FR4)"
PN WO9201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnert TP;
DR WPI; 92-056862/07.
DR P-PSDB; R22586.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 38; Fig 44; 209pp; English.
CC The sequence encodes an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC against NP were separately amplified and reassembled to form the
CC construct, which was then ligated into the fd gene III contg. vec-
CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
CC into fdDOGKan (fdCAT2 with the tet gene replaced by a kanamycin
CC resistance gene) to give fdDOGKanscFvB18, or into the phagemid
CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
CC the effect of using mutator strains to increase the diversity of
CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
CC After 4 rounds of mutation and screening, 40 phage inserts were
CC sequenced. They each displayed single mutations in 6 different
CC positions, five being in the light chain region. More than 70% of
CC the mutations occurred at positions 724 and 725 changing the first
CC Gly in the J segment (framework 4) to Ser (in 21 cases),or Asp (in
CC 3 cases as shown here). The mutant fragments had affinities for
CC NP which were comparable to the wild-type scFv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
CC 736-738, and 793-863.
SQ Sequence 770 BP; 189 A; 197 C; 213 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
Residue Identity = 79% Matches = 288 Mismatches = 65

```
Gaps            =     11  Conservative Substitutions          =      0

                      X       10        20        30        40        50
                      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                      ||| | |||||||||||||||||| |||||||||||||| ||||| |||||
   TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
           10        20 X      30        40        50        60        70

          60        70        80        90       100       110       120
   AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
   ||| |||||||||  |||||||||| || | | |    |  ||  |||||||||||||||||||||||| |
   AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
         80        90       100       110       120       130       140

      130       140       150       160       170       180       190
   CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
   |  ||||| ||||||||||||||||||||||||   ||||| | |||||| ||  |   ||||||| ||  |
   CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
      150       160       170       180       190       200       210

     200       210       220       230       240       250       260
   AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
   ||||||||  | || |  ||||   |||||| ||||||||  ||||||||||||||||||||||||||||||
   AAGGCCACACTGACTGTAGACAAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
    220       230       240       250       260       270       280

   270       280       290       300       310       320       330
   ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
    |||| ||||| || ||||| |||   || |  ||  ||| | ||    ||  || | |||| |||||||||
   TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
  290       300       310       320       330               340       350

     340       350         X
   AGGGACCACGGTCACCGTCTCCTCA
   |||||||||||||||||||||||||
   AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
      360       370       380       390       400       410       420

   GGC
```

8. US-07-977-702-1 (1-360)
   Q23861 ScFvB18 construct mutant #4.

```
ID   Q23861 standard; DNA; 770 BP.
AC   Q23861;
DT   21-MAY-1992  (first entry)
DE   ScFvB18 construct mutant #4.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1..770
FT   /*tag=  a
FT   /product= scFvB18
FT   mutation        724
FT   /*tag=  b
FT   /note= "g -> a; Gly -> Ser (VL FR4)"
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
```

PR 08-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnert TP;
DR WPI; 92-056862/07.
DR P-PSDB; R22585.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 38; Fig 44; 209pp; English.
CC The sequence encodes an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC against NP were separately amplified and reassembled to form the
CC construct, which was then ligated into the fd gene III contg. vec-
CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
CC into fdDOGKan (fdCAT2 with the tet gene replaced by a kanamycin
CC resistance gene) to give fdDOGKanscFvB18, or into the phagemid
CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
CC the effect of using mutator strains to increase the diversity of
CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
CC After 4 rounds of mutation and screening, 40 phage inserts were
CC sequenced. They each displayed single mutations in 6 different
CC positions, five being in the light chain region. More than 70% of
CC the mutations occurred at positions 724 and 725 changing the first
CC Gly in the J segment (framework 4) to Ser (in 21 cases, as shown
CC here) or Asp (in 3 cases). The mutant fragments had affinities
CC for NP which were comparable to the wild-type scFv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
CC 736-738, and 793-863.
SQ Sequence 770 BP; 189 A; 197 C; 213 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
Residue Identity = 79% Matches = 288 Mismatches = 65
Gaps = 11 Conservative Substitutions = 0

```
                    X       10        20        30        40        50
                    GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                    ||| | ||||||||||||||||| |||||||||||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
        10        20 X      30        40        50        60        70

       60        70        80        90       100       110       120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| |||||||||  |||||||||| || | | |    |  ||  |||||||||||||||||||||||| |
AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
      80        90       100       110       120       130       140

      130       140       150       160       170       180       190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
|  ||||| |||||||||||||||||||||||   ||||| | ||||||  ||  |   |||||||  ||  |
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
   150       160       170       180       190       200       210

     200       210       220       230       240       250       260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||||  | || |  ||||   ||||||  ||||||||   ||||||||||||||||||||||||||||
AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
 220       230       240       250       260       270       280
```

```
   270       280       290       300       310       320       330
   ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
    |||| ||||| || ||||| |||   || |  ||  ||| | ||    ||  || | |||| |||||||||
   TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
  290       300       310       320       330               340       350

     340       350         X
   AGGGACCACGGTCACCGTCTCCTCA
   |||||||||||||||||||||||||
   AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
       360       370       380       390       400       410       420

   GGC
```

9. US-07-977-702-1 (1-360)
   Q23860 ScFvB18 construct mutant #3.

```
 ID   Q23860 standard; DNA; 770 BP.
 AC   Q23860;
 DT   21-MAY-1992  (first entry)
 DE   ScFvB18 construct mutant #3.
 KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
 KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
 KW   specific binding pairs; replicable genetic display package; ds.
 OS   Synthetic.
 FH   Key             Location/Qualifiers
 FT   CDS             1..770
 FT   /*tag=  a
 FT   /product= scFvB18
 FT   mutation        706
 FT   /*tag=  b
 FT   /note= "a -> g; Ser -> Gly (VL CDR3)"
 PN   WO9201047-A.
 PD   23-JAN-1992.
 PF   10-JUL-1991; G01134.
 PR   10-JUL-1990; GB-015198.
 PR   19-OCT-1990; GB-022845.
 PR   12-NOV-1990; GB-024503.
 PR   06-MAR-1991; GB-004744.
 PR   15-MAY-1991; GB-010549.
 PA   (CAMB-) CAMBRIDGE ANTIBODY.
 PA   (MEDI-) MED RES COUNCIL.
 PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
 PI   Winter GP, Bonnert TP;
 DR   WPI; 92-056862/07.
 DR   P-PSDB; R22584.
 PT   Producing members of specific binding pairs - by expression in
 PT   recombinant host cells with a secreting replicable genetic
 PT   display package.
 PS   Example 38; Fig 44; 209pp; English.
 CC   The sequence encodes an antibody scFv fragment directed against 4-
 CC   hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
 CC   against NP were separately amplified and reassembled to form the
 CC   construct, which was then ligated into the fd gene III contg. vec-
 CC   tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
 CC   the scFvB18 sequence (see Q21100) fused in frame to gene III was
 CC   designated fdCAT2scFvB18. Alternatively the fragment was cloned
 CC   into fdDOGKan (fdCAT2 with the tet gene replaced by a kanamycin
 CC   resistance gene) to give fdDOGKanscFvB18, or into the phagemid
 CC   pHEN1 to create pHEN1-scFvB18. The constructs were used to test
 CC   the effect of using mutator strains to increase the diversity of
 CC   the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
 CC   NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
```

CC After 4 rounds of mutation and screening, 40 phage inserts were
CC sequenced. They each displayed single mutations in 6 different
CC positions, five being in the light chain region. More than 70% of
CC the mutations occurred at positions 724 and 725 changing the first
CC Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in
CC 3 cases). The mutant shown here (see feature table for details of
CC mutation) occurred once. The mutant fragments had affinities for
CC NP which were comparable to the wild-type scFv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also 021092-100, 103-116, 126-131; 023463, 465-495, 693-719,
CC 736-738, and 793-863.
SQ Sequence 770 BP; 187 A; 197 C; 215 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
Residue Identity = 79% Matches = 288 Mismatches = 65
Gaps = 11 Conservative Substitutions = 0

```
                    X       10        20        30        40        50
                    GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                    ||| | |||||||||||||||||| ||||||||||||| ||||| |||||
TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
        10        20 X      30        40        50        60        70

       60        70        80        90       100       110       120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| |||||||||  |||||||||| || | | |    |  || |||||||||||||||||||||||| |
AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
      80        90       100       110       120       130       140

    130       140       150       160       170       180       190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
|  ||||| |||||||||||||||||||||||   ||||| | |||||| ||  |   ||||||| ||  |
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
   150       160       170       180       190       200       210

  200       210       220       230       240       250       260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||||  | || |  ||||   |||||| ||||||||   ||||||||||||||||||||||||||||
AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
 220       230       240       250       260       270       280

270       280       290       300       310       320       330
ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
 ||||  |||||  || |||||  |||   || |  ||  ||| | ||    ||  || | ||||  |||||||||
TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
290       300       310       320       330               340       350

  340       350         X
AGGGACCACGGTCACCGTCTCCTCA
|||||||||||||||||||||||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
    360       370       380       390       400       410       420

GGC
```

10. US-07-977-702-1 (1-360)
Q23859 ScFvB18 construct mutant #2.

ID Q23859 standard; DNA; 770 BP.
AC Q23859;
DT 21-MAY-1992 (first entry)
DE ScFvB18 construct mutant #2.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;

```
RW   specific binding pairs; replicable genetic display package; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1..770
FT   /*tag=  a
FT   /product= scFvB18
FT   mutation        703
FT   /*tag=  b
FT   /note= "t -> g; Tyr -> Asp (VL CDR3)"
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
DR   P-PSDB; R22583.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 38; Fig 44; 209pp; English.
CC   The sequence encodes an antibody scFv fragment directed against 4-
CC   hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC   against NP were separately amplified and reassembled to form the
CC   construct, which was then ligated into the fd gene III contg. vec-
CC   tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
CC   the scFvB18 sequence (see Q21100) fused in frame to gene III was
CC   designated fdCAT2scFvB18. Alternatively the fragment was cloned
CC   into fdDOGKan (fdCAT2 with the tet gene replaced by a kanamycin
CC   resistance gene) to give fdDOGKanscFvB18, or into the phagemid
CC   pHEN1 to create pHEN1-scFvB18. The constructs were used to test
CC   the effect of using mutator strains to increase the diversity of
CC   the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
CC   NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
CC   After 4 rounds of mutation and screening, 40 phage inserts were
CC   sequenced. They each displayed single mutations in 6 different
CC   positions, five being in the light chain region. More than 70% of
CC   the mutations occurred at positions 724 and 725 changing the first
CC   Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in
CC   3 cases). The mutant shown here (see feature table for details of
CC   mutation) occurred once. The mutation shown on the fig., of t -> c
CC   would result in the Tyr being replaced by His, contrary to the data
CC   in Table 9 of the specification which indicates that the substn. is
CC   with Asp (i.e. t -> g). The mutant fragments had affinities for NP
CC   which were comparable to the wild-type scFv fragment (20nM).
CC   N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC   See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
CC   736-738, and 793-863.
SQ   Sequence   770 BP;    188 A;    197 C;    215 G;    170 T;

Initial Score    =    236  Optimized Score  =    280  Significance = 16.05
Residue Identity =    79%  Matches          =    288  Mismatches   =    65
Gaps             =     11  Conservative Substitutions              =     0

                      X       10        20        30        40        50
                      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                      ||| | ||||||||||||||||| ||||||||||||| ||||| |||||
   TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
         10        20 X      30        40        50        60        70
```

```
       60        70        80        90       100       110       120
AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
||| |||||||||  |||||||||| || | | |    |  ||  |||||||||||||||||||||||| |
AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
      80        90       100       110       120       130       140

    130       140       150       160       170       180       190
CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
|  ||||| |||||||||||||||||||||||||   ||||| | ||||||  ||  |   |||||||  ||  |
CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
   150       160       170       180       190       200       210

  200       210       220       230       240       250       260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||||  | || |  ||||   ||||||  ||||||||   ||||||||||||||||||||||||||||
AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
 220       230       240       250       260       270       280

270       280       290       300       310       320       330
ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
 ||||  |||||  || |||||  |||   || |  ||  |||  | ||    ||  || | ||||  |||||||||
TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
290       300       310       320       330               340       350

  340       350         X
AGGGACCACGGTCACCGTCTCCTCA
|||||||||||||||||||||||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
    360       370       380       390       400       410       420

GGC
```

11. US-07-977-702-1 (1-360)
    Q21100 ScFvB18 construct.

```
ID   Q21100 standard; DNA; 770 BP.
AC   Q21100;
DT   21-MAY-1992  (first entry)
DE   ScFvB18 construct.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1..770
FT   /*tag=  a
FT   /product= scFvB18
FT   mutation        308
FT   /*tag=  b
FT   /note= "c -> t; Ala -> Val (VH FR3); Q23858"
FT   mutation        703
FT   /*tag=  c
FT   /note= "t -> g; Tyr -> Asp (VL CDR3); Q23859"
FT   mutation        706
FT   /*tag=  d
FT   /note= "a -> g; Ser -> Gly (VL CDR3); Q23860"
FT   mutation        724
FT   /*tag=  e
FT   /note= "g -> a; Gly -> Ser (VL FR4); Q23861"
FT   mutation        725
FT   /*tag=  f
FT   /note= "g -> a; Gly -> Asp (VL FR4); Q23862"
FT   mutation        734
```

FT /*tag= "g
FT /note= "c -> t; Thr -> Ile (VL FR4); Q23863"
PN WO9201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; GO1134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CAMB-) CAMBRIDGE ANTIBODY.
PA (MEDI-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnert TP;
DR WPI; 92-056862/07.
DR P-PSDB; R22568.
PT Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 38; Fig 44; 209pp; English.
CC The sequence encodes an antibody scFv fragment directed against 4-
CC hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC against NP were separately amplified and reassembled to form the
CC construct, which was then ligated into the fd gene III contg. vec-
CC tor, fdCAT2, derived from fdTPs/Xh.(See Q21095). The clone having
CC the scFvB18 sequence fused in frame to gene III was designated
CC fdCAT2scFvB18. Alternatively the fragment was cloned into fdDOGKan
CC (fdCAT2 with the tet gene replaced by a kanamycin resistance gene)
CC to give fdDOGKanscFvB18, or into the phagemid pHEN1 to create pHEN1-
CC scFvB18. The constructs were used to test the effect of usingmuta-
CC tor strains to increase the diversity of the cloned genes. The
CC strains NR9046mutD5: NR9046 mutD5::Tn10 and NR9046mutT1: NR9046
CC mutT1::Tn10 were constructed by P1 transduction. After 4 rounds of
CC mutation and screening, 40 phage inserts were sequenced. They each
CC displayed single mutations in 6 different positions, five being in
CC the light chain region. More than 70% of the mutations occurred at
CC positions 724 and 725 changing the first Gly in the J segment
CC (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The
CC mutant fragments had affinities for NP which were comparable to the
CC wild-type scFv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also Q21092-99, 103-116, 126-131; Q23463, 465-495, 693-719,
CC 736-738, and 793-863.
SQ Sequence 770 BP; 188 A; 197 C; 214 G; 171 T;

Initial Score = 236 Optimized Score = 280 Significance = 16.05
Residue Identity = 79% Matches = 288 Mismatches = 65
Gaps = 11 Conservative Substitutions = 0

```
                      X       10        20        30        40        50
                      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                      ||| | ||||||||||||||||||  ||||||||||||||  |||||  |||||
   TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
           10        20 X      30        40        50        60        70

          60        70        80        90        100       110       120
   AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
   ||| |||||||||  ||||||||||  || | | |    |  ||  |||||||||||||||||||||||||| |
   AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
         80        90        100       110       120       130       140

      130       140       150       160       170       180       190
   CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
   |  ||||| ||||||||||||||||||||||||   ||||| | ||||||  ||  |   |||||||  ||  |
   CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
```

```
   150       160       170       180       190       200       210

   200       210       220       230       240       250       260
AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
||||||||  | || |  ||||   |||||| ||||||||   ||||||||||||||||||||||||||||
AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
 220       230       240       250       260       270       280

270       280       290       300       310       320       330
ACTGCCGTCTACTACTGTGC-AGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
 ||||  |||||  ||  |||||  |||   ||  |   ||  |||  | ||    ||  ||  | ||||  |||||||||
TCTGCGGTCTATTATTGTGCAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
290       300       310       320       330               340       350

   340       350       X
AGGGACCACGGTCACCGTCTCCTCA
|||||||||||||||||||||||||
AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
    360       370       380       390       400       410       420

GGC
```

12. US-07-977-702-1 (1-360)
    Q23858 ScFvB18 construct mutant #1.

```
ID   Q23858 standard; DNA; 770 BP.
AC   Q23858;
DT   21-MAY-1992  (first entry)
DE   ScFvB18 construct mutant #1.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package; ds.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   CDS             1..770
FT   /*tag=  a
FT   /product= scFvB18
FT   mutation        308
FT   /*tag=  b
FT   /note= "c -> t; Ala -> Val (VH FR3)"
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
DR   P-PSDB; R22582.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 38; Fig 44; 209pp; English.
CC   The sequence encodes an antibody scFv fragment directed against 4-
CC   hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb
CC   against NP were separately amplified and reassembled to form the
CC   construct, which was then ligated into the fd gene III contg. vec-
CC   tor, fdCAT2, derived from fdTPs/Xh.(See Q21095).  The clone having
```

CC the scFvB18 sequence (see Q21100) fused in frame to gene III was
CC designated fdCAT2scFvB18. Alternatively the fragment was cloned
CC into fdDOGKan (fdCAT2 with the tet gene replaced by a kanamycin
CC resistance gene) to give fdDOGKanscFvB18, or into the phagemid
CC pHEN1 to create pHEN1-scFvB18. The constructs were used to test
CC the effect of using mutator strains to increase the diversity of
CC the cloned genes. The strains NR9046mutD5: NR9046 mutD5::Tn10 and
CC NR9046mutT1: NR9046mutT1::Tn10 were constructed by P1 transduction.
CC After 4 rounds of mutation and screening, 40 phage inserts were
CC sequenced. They each displayed single mutations in 6 different
CC positions, five being in the light chain region. More than 70% of
CC the mutations occurred at positions 724 and 725 changing the first
CC Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in
CC 3 cases). The mutant shown here (see feature table for details of
CC mutation) occurred three times. The mutant fragments had affinities
CC for NP which were comparable to the wild-type scFv fragment (20nM).
CC N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1.
CC See also Q21092-100, 103-116, 126-131; Q23463, 465-495, 693-719,
CC 736-738, and 793-863.
SQ Sequence 770 BP; 188 A; 196 C; 214 G; 172 T;

Initial Score = 234 Optimized Score = 279 Significance = 15.90
Residue Identity = 78% Matches = 287 Mismatches = 66
Gaps = 11 Conservative Substitutions = 0

```
                      X       10        20        30        40        50
                      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTC
                      ||| | |||||||||||||||| |||||||||||||| ||||| |||||
   TTCTATTCTCACAGTGCACAGGTCCAGCTGCAGCAGTCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTG
           10        20 X      30        40        50        60        70

         60        70        80        90       100       110       120
   AAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAA
   ||| |||||||||  |||||||||| || | | |    | ||  |||||||||||||||||||||||| |
   AAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGA
         80        90       100       110       120       130       140

      130       140       150       160       170       180       190
   CAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTC
   |  ||||| |||||||||||||||||||||||||   ||||| | |||||| ||  |   ||||||| ||  |
   CGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGC
      150       160       170       180       190       200       210

     200       210       220       230       240       250       260
   AAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGAC
   ||||||||  | || |  ||||   |||||| ||||||||   ||||||||||||||||||||||||||||
   AAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC
    220       230       240       250       260       270       280

   270       280       290       300       310       320       330
   ACTGCCGTCTACTACTGTG-CAGA-CGGAATGTGG--GTATCAACGGGATATGCTCTGGACTTCTGGGGCCA
    ||||  |||||  || ||||  |||   || |  ||  ||| | ||    ||  || | |||| |||||||||
   TCTGCGGTCTATTATTGTGTAAGATACGACTACGGTAGTAGCTAC----TA--CT-TTGACTACTGGGGCCA
  290       300       310       320       330              340       350

     340       350         X
   AGGGACCACGGTCACCGTCTCCTCA
   |||||||||||||||||||||||||
   AGGGACCACGGTCACCGTCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCCCA
      360       370       380       390       400       410       420

   GGC
```

13. US-07-977-702-1 (1-360)

Q15164 VH186 region of anti-nitrophenylacetyl heavy chain

ID Q15164 standard; DNA; 458 BP.
AC Q15164;
DT 16-MAR-1992 (first entry)
DE VH186 region of anti-nitrophenylacetyl heavy chain Ab gene.
KW mouse; murine; antibody; heavy chain; variable region;
KW polymerase chain reaction; ss.
OS Mus musculus.
PN J03247283-A.
PD 05-NOV-1991.
PF 29-DEC-1989; 340628.
PR 29-DEC-1989; JP-340628.
PA (MATU) MATSUSHITA ELEC IND KK.
DR WPI; 91-366330/50.
PT DNA binding to termini of anti-nitrophenyl:acetyl antibody gene
PT - allows specific amplification of variable region in gene by PCR
PS Disclosure; Page 2; 3pp; Japanese.
CC This sequence corresponds to the region of the heavy chain variable
CC region of the murine anti-nitrophenylacetyl IgG antibody which is
CC amplified by PCR primers HA and HS.
CC See Q15159-Q15163.
SQ Sequence 458 BP; 112 A; 124 C; 120 G; 102 T;

Initial Score = 233 Optimized Score = 277 Significance = 15.83
Residue Identity = 78% Matches = 283 Mismatches = 72
Gaps = 7 Conservative Substitutions = 0

```
                                                X       10        20
                                                GTCAAACTGCAGCAGTCTGGGG
                                                ||| |||||||||||| ||||||
    GCTGTATCATGCTCTTCTTGGCAGCAACAGCTACAGGTGTCCACTCCCAGGTCCAACTGCAGCAGCCTGGGG
            20        30        40        50        60        70        80

          30        40        50        60        70        80        90
    CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
    | ||||||||||||||| ||||| ||||| ||| ||||||||| |||||||||| || | | |    | ||
    CTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTGTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACT
          90        100       110       120       130       140       150

       100       110       120       130       140       150       160
    ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
      |||||||||||||||||||||||| ||  ||||| ||||||||||||||||||||||||   ||||| |
    GGATGCACTGGGTGAAGCAGAGGCCTGGACGAGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTG
       160       170       180       190       200       210       220

     170       180       190       200       210       220       230
    ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
     |||||| ||  |  ||||||| ||  ||||||||| | || |  ||||   |||||| ||||||||
    GTACTAAGTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTACA
     230       240       250       260       270       280       290

   240       250       260       270       280       290       300       310
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
    |||||||||||||||||||||||||||||| |||| ||||| || ||||||    || |  |  || | ||||
    TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCA---AGA-TACGATTA-CTACGG
   300       310       320       330       340           350         360

           320       330       340       350         X
    GATATGCT-CT-GGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
     |   ||| ||  |||| |||||||||||| |||||  |||| |||||||||
    TAGTAGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAAAACAACAGCCCCATC
      370       380       390       400       410       420       430

    GGTCTATCCACTGGCCCCTGT
    440       450
```

14. US-07-977-702-1 (1-360)
    Q06227   VH domain of antibody C against tumour-associated

ID Q06227 standard; DNA; 345 BP.
AC Q06227;
DT 22-JAN-1991 (first entry)
DE VH domain of antibody C against tumour-associated antigens.
KW Tumour-associated antigen; murine monoclonal antibody C;
KW pancreatic carcinoma; metastases; diagnosis; ss.
OS Mus musculus.
PN EP-388914-A.
PD 26-SEP-1990.
PF 21-MAR-1990; 105322.
PR 24-MAR-1989; DE-909799.
PA (BEHW) BEHRINGWERKE AG.
PI Bosslet K, Seemann G, Sedlacek HH;
DR WPI; 90-291873/39.
DR P-PSDB; R07320.
PT Monoclonal antibodies to tumour associated antigens - used for
PT diagnosis of malignant tumours etc.
PS Disclosure; Page 13; 18pp; German.
CC Antibody C is produced as described in EP-141079 and binds to
CC pancreatic carcinoma primary tumours and metastases.
CC They are useful in tumour diagnosis and therapy.
CC See also Q06228 for VK of MAb C, Q07312-15 for MAb A and B and
CC Q06229-30 for MAb D.
SQ Sequence 345 BP; 87 A; 87 C; 93 G; 78 T;

Initial Score = 229 Optimized Score = 245 Significance = 15.53
Residue Identity = 71% Matches = 255 Mismatches = 86
Gaps = 15 Conservative Substitutions = 0

```
      X       10        20        30        40        50        60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||| ||||||||||||||||  | ||||| || ||||| ||||| ||||| ||| |||||||||  |||
   CAGGTCCAACTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGTCCTGCAAGGCT
      X    10        20        30        40        50        60        70

  70        80        90       100       110       120       130       140
   TCTGGCTTCAACATT-AAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGAT
   ||||| | | ||||| |   ||     ||| |||||||||||| |||| |||||  |||||||| ||||||||
   TCTGGATAC-ACATTCACTTACTATGTTATTCACTGGGTGAAACAGAAGCCTGGGCAGGGCCTTGAGTGGAT
         80        90       100       110       120       130       140

          150       160       170       180       190       200       210
   TGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGC
   ||||   ||| |||||   | ||  | |||| | ||  |   ||||||| | | |||||||||  | ||  |
   TGGATACATTCATCCTTACAATGCTGGTACTGAGTACAATGAGAAGTTCAAAGGCAAGGCCACACTGACTTC
       150       160       170       180       190       200       210

        220       230       240       250       260       270       280
   GGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTG
    ||||  ||||||| ||||||||   || ||||||||||||||| ||||||||| |||| ||||| |||||
   AGACAAATCCTCCAGCACAGCCTACATGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTG
     220       230       240       250       260       270       280

      290       300       310       320       330       340       350    X
   TGCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTC
   | || | || | | |||  |     |  ||  ||  || |    ||| ||| ||   ||| ||| || ||
   TTCA-ATGGGACGAGGGGGT-----GACTA--CTGGGGCC--AAGGGACCACGG--TCACCGTCTCC-TCA
   290       300            310           320       330         340     X

    360
   CTCA
```

15. US-07-977-702-1 (1-360)
N91482 Genomic to cDNA junction (V47 to VB1-8) DNA

ID N91482 standard; DNA; 349 BP.
AC N91482;
DT 28-FEB-1990 (first entry)
DE Genomic to cDNA junction (V47 to VB1-8) DNA
KW Human immunodeficiency virus.
OS
PN WO8909393-A.
PD 05-OCT-1989.
PF 20-MAR-1989; U01152.
PR 24-MAR-1988; US-173231.
PA (IGEN) Igen Inc.
PI Kenten JH, Casadei J, Well MJ;
DR WPI; 89-309634/42.
PT New luminescent chimeric proteins - useful in highly sensitive
PT immunoassays, eg for HIV
PS Disclosure; page 35; 79pp; English.
CC This is used in a vector to express the chimeric variable
CC 4-hydroxy-3-nitrophenyl (NP) antigen/aequorin protein, in J558L
CC myeloma cells or other cells expressing lambda 1 light chain.
CC This protein is used as a diagnostic.
SQ Sequence 349 BP; 87 A; 88 C; 96 G; 78 T;

Initial Score = 228 Optimized Score = 269 Significance = 15.46
Residue Identity = 77% Matches = 275 Mismatches = 71
Gaps = 7 Conservative Substitutions = 0

```
          10        20        30        40        50        60        70
   GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCT
            |||||| ||||||| |||||||||||||| ||||| ||||| ||| |||||||||  ||||||
            CAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTGTCCTGCAAGGCTTCT
            X       10        20        30        40        50        60

         80        90       100       110       120       130       140
   GGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGA
   |||| || | | |    | ||  ||||||||||||||||||||||||||| ||  ||||| ||||||||||||
   GGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGACGAGGCCTTGAGTGGATTGGA
        70        80        90       100       110       120       130

      150       160       170       180       190       200       210
   AGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGAC
   ||||||||||||   ||||| | |||||| ||  |   ||||||| ||  |||||||||  | || |  |||
   AGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGAC
     140       150       160       170       180       190       200

    220       230       240       250       260       270       280
   ACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCA
   |   ||||||| ||||||||   |||||||||||||||||||||||||||||| |||| ||||| || ||||||
   AAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCA
   210       220       230       240       250       260       270

  290       300       310       320       330       340       350
   GACGGAATGTGGGTATCAACGGGATATGCT-CT-GGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCT
      || |  |  || | |||| |   ||| ||  |||| ||||||||||||| |||||  |||| |||||||
   ---AGA-TACGATTA-CTACGGTAGTAGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCT
    280       290       300       310       320       330       340

  360
   CA
   ||
   CAG
    X
```

```
> 0 <
0| |0  IntelliGenetics
> 0 <

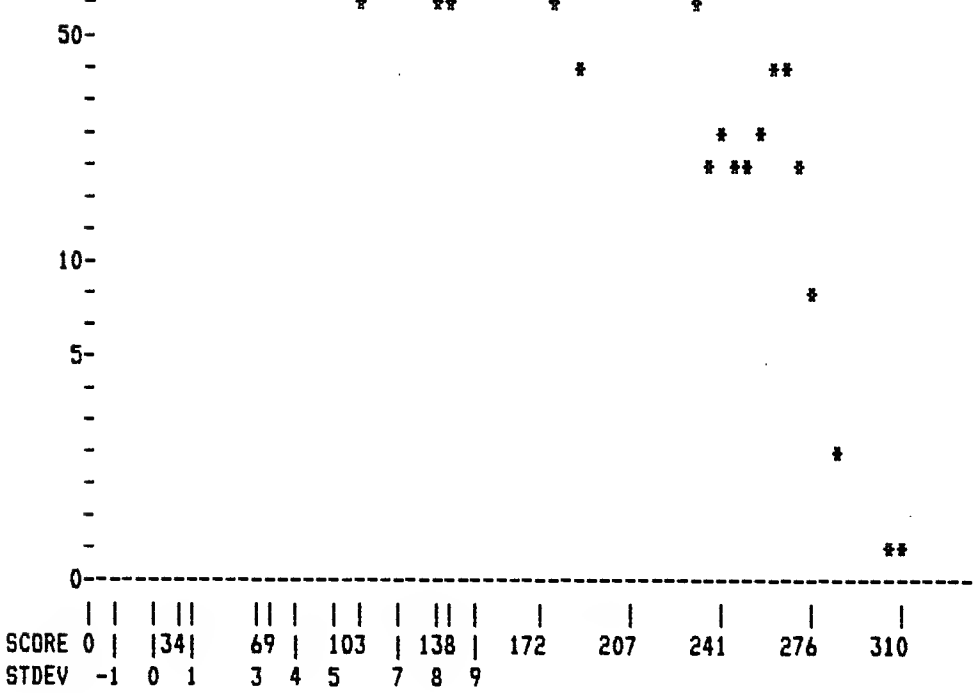
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-977-702-1.res made by shears on Tue 15 Jun 93 12:27:44-PDT.


Query sequence being compared:US-07-977-702-1 (1-360)
Number of sequences searched:               125798
Number of scores above cutoff:                4369

      Results of the initial comparison of US-07-977-702-1 (1-360) with:
   Data bank : EMBL-NEW 3, all entries
   Data bank : GenBank 75, all entries
   Data bank : GenBank-NEW 3, all entries
   Data bank : UEMBL 34_75, all entries

100000-
      -
N     -
U50000-
M     -
B     -
E     -   **
R     -  *
      -     **
0     -
F10000- *     *
      -
S     -
E 5000-        *
Q     -
U     -         *
E     -*
N     -          *
C     -
E     -
S 1000-           *
      -
      -            *
   500-
      -             **
      -                           *
      -
      -                           *
      -               **      *
      -                 ***  *      *             *
   100*                             *  *  * *   *  *
      -                    *  **  *     *    *** *
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	32
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		
Initial scores to save	40	Alignments to save	15
Optimized scores to save	0	Display context	50

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	28	28	13.45

Times:	CPU	Total Elapsed
	00:30:37.12	01:03:42.00

Number of residues: 150464018
Number of sequences searched: 125798
Number of scores above cutoff: 4369

Cut-off raised to 22.
Cut-off raised to 26.
Cut-off raised to 30.
Cut-off raised to 33.
Cut-off raised to 36.
Cut-off raised to 39.
Cut-off raised to 41.
Cut-off raised to 44.
Cut-off raised to 46.
Cut-off raised to 49.
Cut-off raised to 53.
Cut-off raised to 58.
Cut-off raised to 64.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 20 standard deviations above mean ****					
1. MMIGGNP2	Mouse mRNA for idiotypic anti	420	310	318	20.97	0
2. MMCEAHCH	M.musculus gene for anti-CEA	861	309	316	20.89	0
3. MUSIGHNPA	Mouse Ig active H-chain mRNA,	421	305	318	20.60	0
	**** 18 standard deviations above mean ****					
4. MUSIGHNP	Mouse Ig active H-chain mRNA,	414	281	314	18.81	0
5. MMIGGNP1	Mouse mRNA for idiotypic anti	414	281	314	18.81	0
6. MMV20292B	M.musculus mRNA for VH-gen se	363	276	282	18.44	0
7. S114902	immunoglobulin heavy chain (n	452	276	281	18.44	0
8. MMIGVDJAA	M.musculus immunoglobulin hea	452	276	281	18.44	0
9. MUSIGHNPG	Mouse Ig active H-chain mRNA,	414	273	309	18.22	0
10. MMIGGNP8	Mouse mRNA for idiotypic anti	414	273	307	18.22	0
11. MUSIGHNPB	Mouse Ig active H-chain mRNA,	414	272	307	18.14	0
12. MMIGGNP3	Mouse mRNA for idiotypic anti	414	272	308	18.14	0
13. MMIGG1HCV	M.musculus rearranged mRNA fo	351	271	316	18.07	0
14. MUSIGMU4G	Mouse monoclonal antiidiotypi	354	271	307	18.07	0
15. MUSIGHBB	Mouse Ig active mu-chain VDJ-	390	271	326	18.07	0
16. MUSIGHBH	Mouse Ig active H-chain: anti	501	271	324	18.07	0
17. MMIGVK1	Mouse mRNA for anti-GAT VH an	501	271	324	18.07	0
18. MUSIGHXO	Mouse Ig germline H-chain gen	970	271	305	18.07	0
19. MMIG10VH	Mouse (GAT-specific) subgroup	970	271	305	18.07	0
20. MMIGHVXA	Mouse (hybridoma 3A112) immun	1069	271	277	18.07	0
21. MUSIGHVXA	Mouse (hybridoma 3A112) immun	1069	271	277	18.07	0
	**** 17 standard deviations above mean ****					
22. MMV20311	M.musculus mRNA for VH-gen se	363	270	279	17.99	0
23. MUSIGHADE	Mouse Ig rearranged H-chain g	404	270	275	17.99	0
24. MUSIGHEA	Mouse Ig mu-chain active V-re	444	269	322	17.92	0
25. MUSIGHDZ	Mouse Ig mu-chain active V-re	444	269	322	17.92	0
26. MUSIGHNPH	Mouse Ig active H-chain mRNA,	417	268	321	17.85	0
27. MUSIGHBC	Mouse Ig active H-chain a-NP	511	268	321	17.85	0
28. MUSIGHZTA	Mouse Ig germline H-chain gen	294	267	272	17.77	0
29. MUSIGHZP	Mouse Ig germline H-chain gen	294	266	271	17.70	0
30. MUSIGHAEM	Mouse Ig heavy-chain mRNA V r	328	266	288	17.70	0
31. MUSIGB1H1	Mouse mRNA for immunoglobulin	1544	266	271	17.70	0
32. MMIGB1H1	Mouse mRNA for immunoglobulin	1544	266	271	17.70	0
33. MUSIGHZQ	Mouse Ig germline H-chain gen	291	265	268	17.62	0
34. MUSIGHZN	Mouse Ig germline H-chain gen	291	265	267	17.62	0
35. MUSIGHDF	Mouse Ig active mu-chain V-re	363	265	271	17.62	0
36. MMIGNP4	Mouse mRNA for idiotypic anti	411	265	310	17.62	0
37. MUSIGHNPE	Mouse Ig active H-chain mRNA,	417	265	312	17.62	0
38. MMIGGNP6	Mouse mRNA for idiotypic anti	417	265	312	17.62	0
39. MMIGWM65B	M.musculus WM65 immunoglobuli	536	265	317	17.62	0
40. MMIGHVXZ	Mouse (hybridoma H1-39) immun	1068	265	273	17.62	0

1. US-07-977-702-1 (1-360)
   MMIGGNP2 Mouse mRNA for idiotypic anti-NP IgG(1) heavy chai

```
LOCUS       MMIGGNP2      420 bp    RNA             ROD       07-MAY-1992
DEFINITION  Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-D-J
            (hybridoma 18.1.16)
ACCESSION   X02563 M12744
KEYWORDS    gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin;
            joining region; signal peptide; variable region.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 420)
```

```
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region: Multiple gene segments encode
            anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
COMMENT     *source: strain=Balb/c;

            Serological analysis of hybridomaproteins resulting from the immune
            response to the hapten NP reveals NP(a) idiotypes expressed by
            Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The
            NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV
            sharing more determinants than V and VI which appear quite
            distinct.
FEATURES             Location/Qualifiers
     sig_peptide     1..57
     mat_peptide     join(58..351,352..375,376..420)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
     misc_feature    58..351
                     /note="variable region (aa 1-98)"
     misc_feature    148..162
                     /note="CDR I"
     misc_feature    205..255
                     /note="CDR II"
     misc_feature    352..375
                     /note="D-region (aa 99-106)"
     misc_feature    376..>420
                     /note="J-region (aa 107-121)"
     CDS             join(1..351,352..375,376..420)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
                     /codon_start=1
                     /translation="MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTAS
                     GFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQL
                     SSLTSEDTAVYYCARYLYYYGSSDFDYWGQGTTLTVSS"
BASE COUNT      107 a    106 c    110 g     97 t
ORIGIN

Initial Score    =    310  Optimized Score  =    318  Significance = 20.97
Residue Identity =    88%  Matches          =    323  Mismatches   =    34
Gaps             =      6  Conservative Substitutions               =     0

                                                  X       10        20
                                                  GTCAAACTGCAGCAGTCTGGGG
                                                  ||  | ||||||||||||||||
   GCTGGGTTATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
           20        30        40        50        60        70        80

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
         90        100       110       120       130       140       150

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
      160       170       180       190       200       210       220

    170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
   |||||||||||||||||||||||||| |||||||||||| ||||| ||||| ||||||||||||||||  |
   ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
    230       240       250       260       270       280       290

  240       250       260       270       280       290       300
```

```
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGA---TACCTCTATTACTACG
  300       310       320       330       340       350          360

  310         320       330       340       350         X
    GGA-TA-TGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
    | | ||  |   | |||| |||||||||||| |||||  |||| |||||||||
    GTAGTAGCGACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA
    370       380       390       400       410       420
```

2. US-07-977-702-1 (1-360)
   MMCEAHCH M.musculus gene for anti-CEA mAb T84.66 heavy chai

```
 LOCUS       MMCEAHCH      861 bp    DNA             ROD       03-DEC-1992
 DEFINITION  M.musculus gene for anti-CEA mAb T84.66 heavy chain V-region
 ACCESSION   X52769
 KEYWORDS    CEA; heavy chain; tumor-associated antigen.
 SOURCE      mouse
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 861)
   AUTHORS   Neumaier,M., Shively,L., Chen,F.S., Gaida,F.J., Ilgen,C.,
             Paxton,R.J., Shively,J.E. and Riggs,A.D.
   TITLE     Cloning of the genes for T86.66, an antibody that has a high
             specificity and affinity for carcinoembryonic antigen, and
             expression of chimeric human/mouse T84.66 genes in myeloma and
             Chinese hamster ovary cells
   JOURNAL   Cancer Res. 50, 2128-2134 (1990)
   STANDARD  full automatic
 FEATURES             Location/Qualifiers
      promoter        109..118
      promoter        121..127
      promoter        160..166
      promoter        169..176
      exon            272..317
                      /number=1
      exon            396..770
                      /number=2
      intron          318..395
                      /number=1
      CDS             join(272..317,396..770)
                      /partial
                      /note="heavy chain"
                      /product="anti-CEA mAb T84.66"
                      /codon_start=1
                      /translation="MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVEPGASVKLSCTAS
                      GFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNSKYVPKFQGKATITADTSSNTAYL@L
                      TSLTSEDTAVYYCAPFGYYVSDYAMAYWGQGTSVTVSS"
 BASE COUNT      213 a    208 c    203 g    237 t
 ORIGIN

Initial Score    =    309  Optimized Score  =    316  Significance = 20.89
Residue Identity =    88%  Matches          =    322  Mismatches   =    33
Gaps             =     10  Conservative Substitutions               =     0

                                                 X       10        20
                                                 GTCAAACTGCAGCAGTCTGGGG
                                                 ||  | ||||||||||||||||
   GTGACAGTGGCAATCACTTTGCCTTTCTTTCTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
 360       370       380       390       400       410       420       430

        30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
```

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CAGAGCTTGTGGAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
      440       450       460       470       480       490       500

   100       110       120       130       140       150       160
ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| |||
ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAATGGATTGGAAGGATTGATCCTGCGAATGGTA
    510       520       530       540       550       560       570

  170       180       190       200       210       220       230
ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
||| |||||||| |||||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
ATAGTAAATATGTCCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
  580       590       600       610       620       630       640

 240       250       260       270       280       290       300
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACG-
||||||||| ||||||||||||||||||||||||||||| || |||||   ||   | ||| || | |||
TGCAGCTCACCAGCCTGACATCTGAGGACACTGCCGTCTATTATTGTGC-TCCG---TTTGGTTA-CTACGT
650       660       670       680       690       700           710

  310       320       330       340       350       X
----GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
    |  |||||| ||| || |||||| ||||| ||| | ||||||||||||||||
GTCTGACTATGCTATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGGTAAGAATGGCCTCTC
   720       730       740       750       760       770       780

CAGGTCTTTATTTTTAACCTTTGTATGGACTTT
 790       800       810
```

3. US-07-977-702-1 (1-360)
   MUSIGHNPA Mouse Ig active H-chain mRNA, V-region (VDJ) from

```
LOCUS       MUSIGHNPA     421 bp ss-mRNA            ROD       01-SEP-1988
DEFINITION  Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma
            18.1.16.
ACCESSION   M12744
KEYWORDS    immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE      Mouse (BALB/c) hybridoma 18.1.16, cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region Multiple gene segments encode
            anti-4-(hydroxy-3-nitropheny)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     sig_peptide     1..57
                     /codon_start=1
                     /note="Ig H-chain V-region signal peptide"
     mat_peptide     58..>421
                     /codon_start=1
                     /note="Ig H-chain V-region"
     misc_recomb     351..352
                     /note="V-region end/D-region start"
     misc_recomb     375..376
                     /note="D-region end/J-region start"
     CDS             1..>421
                     /note="Ig H-chain;  (VDJ-region) precursor"
                     /codon_start=1
                     /translation="MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTAS
```

```
                    GFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQL
                    SSLTSEDTAVYYCARYLYYYGSSYFDYWGQGTTLTVSLX*
 BASE COUNT      107 a    106 c    110 g     98 t
 ORIGIN      Chromosome 12.

Initial Score    =    305  Optimized Score  =    318  Significance = 20.60
Residue Identity =    89%  Matches          =    324  Mismatches   =    33
Gaps             =      7  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||||||
    GCTGGGTTATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
            20        30        40        50        60        70        80

          30        40        50        60        70        80        90
    CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
    |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
    CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
          90        100       110       120       130       140       150

       100       110       120       130       140       150       160
    ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
    ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
       160       170       180       190       200       210       220

     170       180       190       200       210       220       230
    ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
    |||||||||||||||||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
    ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
     230       240       250       260       270       280       290

   240       250       260       270       280       290       300
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
    |||||||||||||||||||||||||||||||||||| |||||||| |||    |  |   |  | |||
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGA---TACCTCTATTACTACG
   300       310       320       330       340       350          360

  310       320       330       340       350          X
    GGATATGCT-CT-GGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTC-CTCA
    | |   ||| ||  |||| |||||||||||| |||||  |||| ||||| ||||
    GTAGTAGCTACTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCGCTCA
    370       380       390       400       410       420
```

4. US-07-977-702-1 (1-360)
   MUSIGHNP Mouse Ig active H-chain mRNA, V-region (VDJ) from

```
 LOCUS       MUSIGHNP      414 bp ss-mRNA            ROD       01-SEP-1988
 DEFINITION  Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma
             20.1.43.
 ACCESSION   M12176
 KEYWORDS    immunoglobulin; immunoglobulin heavy chain; variable region.
 SOURCE      Mouse (BALB/c) hybridoma 20.1.43, cDNA to mRNA.
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 414)
   AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
             Imanishi-Kari,T.
   TITLE     Heavy chain variable region Multiple gene segments encode
             anti-4-(hydroxy-3-nitropheny)acetyl idiotypic antibodies
   JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
   STANDARD  full automatic
 FEATURES             Location/Qualifiers
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     sig_peptide     1..57
                     /codon_start=1
                     /note="Ig H-chain V-region signal peptide"
     mat_peptide     58..>414
                     /codon_start=1
                     /note="Ig H-chain V-region"
     misc_recomb     351..352
                     /note="V-region end/D-region start"
     misc_recomb     366..367
                     /note="D-region end/J-region start"
     CDS             1..>414
                     /note="Ig H-chain;  (VDJ-region) precursor"
                     /codon_start=1
                     /translation="MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVRPGASVKLSCTAS
                     GFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQL
                     SSLTSEDTAVYYCASYRYERAWFAYWGQGTLVTVSA"
BASE COUNT      101 a     98 c    118 g     97 t
ORIGIN      Chromosome 12.

Initial Score    =    281  Optimized Score  =    314  Significance = 18.81
Residue Identity =    88%  Matches          =    321  Mismatches   =    31
Gaps             =     10  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||||||
   GCTGGGTTATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
           20        30        40        50        60        70        80

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
         90       100       110       120       130       140       150

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
      160       170       180       190       200       210       220

     170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
   |||||||||||||||||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
   ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
    230       240       250       260       270       280       290

  240       250       260       270       280       290       300
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
   |||||||||||||||||||||||||||||||||||||||| |||||||| ||      | | |||| | |
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAG-----TTATAGGTA-CGAGA
  300       310       320       330       340       350             360

  310       320       330       340       350       360
   GGATATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
   ||   || | ||  ||| ||||||||||||||   |||||| |||||  ||
   GGGCCTGGTTTG--CTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
      370       380       390       400       410   X


5. US-07-977-702-1 (1-360)
   MMIGGNP1     Mouse mRNA for idiotypic anti-NP IgG(1) heavy chai

LOCUS       MMIGGNP1      414 bp    RNA             ROD       07-MAY-1992
DEFINITION  Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-J (hybridoma
            20.1.43)
```

```
ACCESSION   X02582 M12176
KEYWORDS    gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin;
            joining region; signal peptide; variable region.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region: Multiple gene segments encode
            anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
COMMENT     *source: strain=Balb-c;

            Serological analysis of hybridomaproteins resulting from the immune
            response to the hapten NP reveals NP(a) idiotypes expressed by
            Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The
            NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV
            sharing more determinants than V and VI which appear quite
            distinct.
FEATURES             Location/Qualifiers
     sig_peptide     1..57
     misc_feature    58..351
                     /note="variable region (aa 1-98)"
     misc_feature    148..162
                     /note="CDR 1"
     misc_feature    205..255
                     /note="CDR 2"
     misc_feature    352..366
                     /note="D-region (aa 99-103)"
     misc_feature    367..>414
                     /note="J-region (aa 104-119)"
     CDS             join(58..351,352..366,367..414)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-J"
                     /codon_start=1
                     /translation="EVQLQQSGAELVRPGASVKLSCTASGFNIKDTYMHWVKQRPEQG
                     LEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCASYRYE
                     RAWFAYWGQGTLVTVSA"
BASE COUNT      101 a     98 c    118 g     97 t
ORIGIN
```

```
Initial Score    =    281  Optimized Score  =    314  Significance = 18.81
Residue Identity =    88%  Matches          =    321  Mismatches   =    31
Gaps             =     10  Conservative Substitutions               =     0
```

```
                                                  X       10        20
                                                  GTCAAACTGCAGCAGTCTGGGG
                                                  ||  | ||||||||||||||||
   GCTGGGTTATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
           20        30        40        50        60        70        80

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
         90        100       110       120       130       140       150

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
      160       170       180       190       200       210       220

    170       180       190       200       210       220       230
```

```
   ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
   |||||||||||||||||||||||||| |||||||||||| ||||| ||||| ||||||||||||||||  |
   ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
    230       240       250       260       270       280       290

  240       250       260       270       280       290       300
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
   |||||||||||||||||||||||||||||||||||||||| |||||||| ||      | | |||| | |
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAG-----TTATAGGTA-CGAGA
  300       310       320       330       340       350             360

 310       320       330       340       350       360
   GGATATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
   ||   || | ||  ||| ||||||||||||||   |||||| |||||  ||
   GGGCCTGGTTTG--CTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
      370         380       390       400       410   X
```

6. US-07-977-702-1 (1-360)
   MMV20292B M.musculus mRNA for VH-gen sequence of naturally o

```
LOCUS       MMV20292B     363 bp    RNA             ROD       23-JUN-1992
DEFINITION  M.musculus mRNA for VH-gen sequence of naturally occurring,
            somatically mutated memory B cell
ACCESSION   Z12783 X59730
KEYWORDS    somatic mutation.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Schittek,B. and Rajewsky,K.
  TITLE     Natural occurence and origin of somatically mutated memory B cells
            in mice
  JOURNAL   J. Exp. Med. 0, 0-0 (1992)
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 363)
  AUTHORS   Schittek,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUN-1992) B. Schittek, Institut of Genetics, Weyertal
            121, W-5000 Cologne, FRG
  STANDARD  full automatic
COMMENT     *source: strain=C57BL/6;
            *source: haplotype=IgHb;
            *source: stage=Adult;
            *source: tissue=Spleen;
            *source: cell_type=B-cell;
            *source: clone_library=cDNA library specifically amplified;
            *source: clone=V2029_2B;
            *source: isolate=V2029_2B;
            *source: sex=Female;
            *source: is_macronuclear=N;
            *source: is_proviral=N;
            *source: is_germline=N.
BASE COUNT      89 a    91 c   102 g    81 t
ORIGIN
```

```
Initial Score    =   276  Optimized Score  =   282  Significance = 18.44
Residue Identity =   78%  Matches          =   287  Mismatches   =   69
Gaps             =     8  Conservative Substitutions             =     0
```

```
      X       10        20        30        40        50        60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||| |||||||||||| ||||||| |||||||||||||||| ||||| ||||| ||| |||||||||  |||
   CAGGTCCAACTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTGTCCTGCAAGGCT
      X    10        20        30        40        50        60        70
```

```
  70        80        90        100       110       120       130       140
   TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
   ||||||| || | | |    |  ||  ||||||||||||||||||||||||| ||  ||||| |||||||||
   TCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGACGAGGCCTTGAGTGGATT
         80        90        100       110       120       130       140

         150       160       170       180       190       200       210
   GGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCG
   ||||||||||||||   ||||| | |||||| ||  |   ||||||| ||  |||||||||  | || |
   GGAAGGATTGATCCTAATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTA
      150       160       170       180       190       200       210

       220       230       240       250       260       270       280
   GACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGT
   ||||   |||||| ||||||||   ||||||||||||||||||||||||||||| |||| ||||| || |||
   GACAAACCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGT
    220       230       240       250       260       270       280

     290       300           310       320       330       340       350
   GCAGACGGAATGTGGGTAT--CAA--CGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGT
   ||| |  ||   |||||||   ||  |    |||||| |||||| ||||||| ||||| ||| | ||||||||
   GCA-AGAGA---TGGGTATGGTAACTCCCTCTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGT
  290           300       310       320       330       340       350

      360
   CTCCTCA
   |||||||
   CTCCTCA
    360  X
```

7. US-07-977-702-1 (1-360)
   S114902 immunoglobulin heavy chain {nonfunctional VDJ comp

```
LOCUS       S114902       452 bp    DNA             ROD       30-NOV-1992
DEFINITION  immunoglobulin heavy chain {nonfunctional VDJ complex} [mice, pre-B
            cell line 46 transformed with ts mutant of A-MuLV, Genomic, 452 nt]
ACCESSION   S45712
KEYWORDS    .
SOURCE      mice pre-B cell line 46 transformed with ts mutant of A-MuLV
  ORGANISM  Unclassified.
            Unclassified.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Shirasawa,T., Miyazoe,I., Hagiwara,S., Kimoto,H., Shigemoto,K.,
            Taniguchi,M. and Takemori,T.
  TITLE     Heavy chain variable (VH) region diversity generated by VH gene
            replacement in the progeny of a single precursor cell transformed
            with a temperature-sensitive mutant of Abelson murine leukemia
            virus.
  JOURNAL   J. Exp. Med. 176, 1209-1214 (1992)
  STANDARD  full automatic
COMMENT     This entry [NCBI gibbsq 114902] was created by the journal scanning
            component of NCBI/GenBank at the National Library of Medicine.
            This sequence comes from Fig. 2.  The authors begin their numbering
            at -6.  Zero is not present in the numbering.
FEATURES             Location/Qualifiers
     CDS             join(7..52,132..452)
                     /partial
                     /note="Description: immunoglobulin heavy chain"
BASE COUNT      113 a    115 c    115 g    109 t
ORIGIN
```

```
Initial Score    =    276  Optimized Score  =    281  Significance = 18.44
Residue Identity =    91%  Matches          =    284  Mismatches   =    22
Gaps             =      3  Conservative Substitutions              =     0
```

```
                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||||||
   GTGACAGTGGCAATCACTTTGCCTTTCTTTCTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
     100       110       120       130       140     X 150       160

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   170       180       190       200       210       220       230

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
 240       250       260       270       280       290       300       310

    170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
   |||||||||||||||||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
   ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
         320       330       340       350       360       370       380

  240       250       260       270       280       290       300       X
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGG-AATGTGGGTATCAACG
   |||||||||||||||||||||||||||||||||||| |||||||| ||||       |||| |  |
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC-TACGGTTCCCCTGGTA-CTTC
      390       400       410       420       430       440       450 X

 310       320       330       340       350
   GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCT
```

8. US-07-977-702-1 (1-360)
   MMIGVDJAA M.musculus immunoglobulin heavy chain VDJ complex

```
 ID   MMIGVDJAA  standard; DNA; ROD; 452 BP.
 XX
 AC   Z21679;
 XX
 DT   17-FEB-1993 (Rel. 35, Created)
 DT   17-FEB-1993 (Rel. 35, Last updated, Version 1)
 XX
 DE   M.musculus immunoglobulin heavy chain VDJ complex gene.
 XX
 KW   immunoglobulin heavy chain; VDJ complex.
 XX
 OS   Mus musculus (mouse)
 OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC   Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 XX
 RN   [1]
 RP   1-452
 RA   Shirasawa T., Miyazoe I., Hagiwara S., Kimoto H., Shigemoto K.,
 RA   Taniguchi M., Takemori T.;
 RT   "Heavy Chain Variable (VH) Region Diversity Generated by VH Gene
 RT   Replacement in the Progeny of a Single Precursor Cell Transformed
 RT   with a Temperature-sensitive Mutant of Abelson Murine Leukemia
 RT   Virus";
 RL   J. Exp. Med. 176:1209-1214(1992).
 XX
 RN   [2]
 RP   1-452
 RA   Shirasawa T.;
```

```
RT   ;
RL   Submitted (27-JAN-1993) on tape to the EMBL Data Library by:
RL   Takuji Shirasawa, Molecular Pathology, Tokyo Metropolitan Institute
RL   of Gerontology, 35-2 Sakae-cho, Itabashi-ku, Tokyo, 173, Japan
XX
CC   *source: strain=BALB/c;
CC   *source: cell_line=pre-B cell;
CC   *source: clone_library=pre-B cell;
CC   *source: clone=VDJ;
CC   *source: is_macronuclear=N;
CC   *source: is_proviral=N;
CC   *source: is_germline=N;
XX
FH   Key             Location/Qualifiers
FH
FT   exon            7..52
FT                   /number=1
FT   intron          53..131
FT   exon            132..452
FT                   /number=2
FT   CDS             join(7..52,132..>452)
FT                   /product="VDJ complex"
FT   misc_feature    432..439
FT                   /note="D region"
FT   misc_feature    440..442
FT                   /note="N sequence"
FT   misc_feature    443..452
FT                   /note="J region"
XX
SQ   Sequence 452 BP; 113 A; 115 C; 115 G; 109 T; 0 other;

Initial Score    =    276  Optimized Score  =    281  Significance = 18.44
Residue Identity =    91%  Matches          =    284  Mismatches   =    22
Gaps             =      3  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||||||
   GTGACAGTGGCAATCACTTTGCCTTTCTTTCTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
     100       110       120       130       140     X 150       160

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   170       180       190       200       210       220       230

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
 240       250       260       270       280       290       300       310

    170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
   |||||||||||||||||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
   ATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
         320       330       340       350       360       370       380

  240       250       260       270       280       290       300       X
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGG-AATGTGGGTATCAACG
   |||||||||||||||||||||||||||||||||||||| |||||||| ||||       |||| |  |
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC-TACGGTTCCCCTGGTA-CTTC
      390       400       410       420       430       440       450 X

 310       320       330       340       350
```

GGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCCT

9. US-07-977-702-1 (1-360)
MUSIGHNPG Mouse Ig active H-chain mRNA, V-region (VDJ) from

```
LOCUS       MUSIGHNPG     414 bp ss-mRNA            ROD       01-SEP-1988
DEFINITION  Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma
            P3.6.5.
ACCESSION   M12750
KEYWORDS    immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE      Mouse (C57BL/6) group V hybridoma P3.6.5, cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region Multiple gene segments encode
            anti-4-(hydroxy-3-nitropheny)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     sig_peptide     1..57
                     /codon_start=1
                     /note="Ig H-chain V-region signal peptide"
     mat_peptide     58..>414
                     /codon_start=1
                     /note="Ig H-chain V-region"
     misc_recomb     351..352
                     /note="V-region end/D-region start"
     misc_recomb     372..373
                     /note="D-region end/J-region start"
     CDS             1..>414
                     /note="Ig H-chain;  (VDJ-region) precursor"
                     /codon_start=1
                     /translation="MKCSWIMFFLMAVVTGVNSEVQLQQSGAELVRPGASVKLSCTAS
                     GFNIKDTYMHWVKQRTEQGLEWIGRIDPEDGETKYAPKFQVKATITADTSSNTAYLQL
                     SSLTSEDTAVYYCARYYYGSSFFAYWGQGTLVTVSA"
BASE COUNT      103 a     99 c    113 g     99 t
ORIGIN      Chromosome 12.
```

```
Initial Score    =    273  Optimized Score  =    309  Significance = 18.22
Residue Identity =    87%  Matches          =    317  Mismatches   =    34
Gaps             =     12  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||||||
   GCTGGATCATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
           20        30        40        50        60        70        80

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   |||||||||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
   CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTTGTCCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
         90       100       110       120       130       140       150

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |  ||| |
   ATATGCACTGGGTGAAGCAGAGGACTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGAGGATGGTG
      160       170       180       190       200       210       220

    170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
```

```
   | ||||||||| |||||| |||||||||||||||||||| ||||| ||||| |||||||||||||||| |
   AAACTAAATATGCCCCGAAATTCCAGGTCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
    230       240       250       260       270       280       290

  240       250       260       270       280       290       300
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAACG
   |||||||||||||||||||||||||||||||||||| |||||||| |||    ||     || | |||
   TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGA---TAT-----TA-CTACG
  300       310       320       330       340       350                 360

 310       320       330       340       350       360
   GGA-TATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
   | | ||   |||   ||| ||||||||||||||   |||||| |||||  ||
   GTAGTAGCTTCTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
         370       380       390       400       410   X
```

10. US-07-977-702-1 (1-360)
    MMIGGNP8   Mouse mRNA for idiotypic anti-NP IgG(1) heavy chai

```
LOCUS       MMIGGNP8      414 bp    RNA             ROD       07-MAY-1992
DEFINITION  Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-D-J
            (hybridoma P.3.6.5)
ACCESSION   X02569 M12750
KEYWORDS    gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin;
            joining region; signal peptide; variable region.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region: Multiple gene segments encode
            anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
COMMENT     *source: strain=C57BL/6;

            Serological analysis of hybridomaproteins resulting from the immune
            response to the hapten NP reveals NP(a) idiotypes expressed by
            Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The
            NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV
            sharing more determinants than V and VI which appear quite
            distinct.
FEATURES             Location/Qualifiers
     sig_peptide     1..57
     mat_peptide     join(58..147,352..414)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
     misc_feature    58..147
                     /note="V-region (aa 1-98)"
     misc_feature    148..162
                     /note="CDR I"
     misc_feature    205..255
                     /note="CDR II"
     misc_feature    352..372
                     /note="D-region (aa 99-105)"
     misc_feature    373..>414
                     /note="J-region (aa 106-119)"
     CDS             join(1..147,352..414)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
                     /codon_start=1
                     /translation="MKCSWIMFFLMAVVTGVNSEVQLQQSGAELVRPGASVKWSCTAS
                     GFNIKYYYGSSFFAYWGQGTLVTVSA"
BASE COUNT      102 a    100 c    114 g     98 t
ORIGIN
```

```
Initial Score    =    273  Optimized Score  =    307  Significance = 18.22
Residue Identity =    86%  Matches          =    314  Mismatches   =    38
Gaps             =     10  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||||||
    GCTGGATCATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGG
            20        30        40        50        60        70        80

          30        40        50        60        70        80        90
    CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
    |||||||||||| |||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||
    CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTGGTCCTGCACGGCTTCTGGCTTCAACATTAAAGACACCT
        90        100       110       120       130       140       150

       100       110       120       130       140       150       160
    ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
    |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||| |  ||| |
    ATATGCACTGGGTGAAGCAGAGGACTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGAGGATGGTG
       160       170       180       190       200       210       220

     170       180       190       200       210       220       230
    ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
    | ||||||||||| |||||| |||||||||||||||||||| ||||| ||||| |||||||||||||||  |
    AAACTAAATATGCCCCGAAATTCCAGGTCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
     230       240       250       260       270       280       290

   240       250       260       270       280       290       300       310
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
    |||||||||||||||||||||||||||||||||||||||| ||||||||    |  ||     || | ||||
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGC--TAGCTAT-----TA-CTACGG
   300       310       320       330       340         350             360

           320       330       340       350       360
    GA-TATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
     | ||   |||   ||| ||||||||||||||   |||||| |||||  ||
    TAGTAGCTTCTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
         370       380       390       400       410   X
```

11. US-07-977-702-1 (1-360)
    MUSIGHNPB Mouse Ig active H-chain mRNA, V-region (VDJ) from

```
LOCUS       MUSIGHNPB     414 bp ss-mRNA            ROD       01-SEP-1988
DEFINITION  Mouse Ig active H-chain mRNA, V-region (VDJ) from anti-NP hybridoma
            P5.40.1.
ACCESSION   M12745
KEYWORDS    immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE      Mouse (C57BL/6) group VI hybridoma P5.40.1, cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region Multiple gene segments encode
            anti-4-(hydroxy-3-nitropheny)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     sig_peptide     1..57
                     /codon_start=1
                     /note="Ig H-chain V-region signal peptide"
     mat_peptide     58..>414
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                    /codon_start=1
                    /note="Ig H-chain V-region"
     misc_recomb    351..352
                    /note="V-region end/D-region start"
     misc_recomb    371..372
                    /note="D-region end/J-region start"
     CDS            1..>414
                    /note="Ig H-chain;  (VDJ-region) precursor"
                    /codon_start=1
                    /translation="MKFSWVMFFLMAVVTGVNSEVQLQQSVAELVRPGASVKLSCTAS
                    GFNIKNTYMHWVKQRPEQGLEWIGRIDPANGSTKYAPKFQIKATITADTSSNTAYLQL
                    SSLTSEDTAIYYCAPYYYESSLFAYWGQGTLVTVSA"
 BASE COUNT      101 a    104 c    109 g    100 t
 ORIGIN      Chromosome 12.

Initial Score    =    272  Optimized Score  =    307  Significance = 18.14
Residue Identity =    86%  Matches          =    314  Mismatches   =    38
Gaps             =     10  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | ||||||||||||| ||
    GCTGGGTCATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGTGG
            20        30        40        50        60        70        80

          30        40        50        60        70        80        90
    CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
    |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
    CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAAACACCT
          90       100       110       120       130       140       150

       100       110       120       130       140       150       160
    ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
    ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
       160       170       180       190       200       210       220

     170       180       190       200       210       220       230
    ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
     |||||| |||| |||||||||||||| |||||||||||||| ||||| ||||| |||||||||||||||  |
    GTACTAAGTATGCCCCGAAGTTCCAGATCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
     230       240       250       260       270       280       290

   240       250       260       270       280       290       300       310
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
    |||||||||||||||||||||||||||||||||| |||| ||||||||   |   ||     || | |||
    TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCATCTATTACTGTGC--CCCTTAT-----TA-CTACGA
   300       310       320       330       340         350             360

           320       330       340       350       360
    GA-TATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
    || ||  || |   ||| ||||||||||||||   |||||| |||||  ||
    GAGTAGCCTGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
        370       380       390       400       410   X


12. US-07-977-702-1 (1-360)
    MMIGGNP3     Mouse mRNA for idiotypic anti-NP IgG(1) heavy chai

 LOCUS       MMIGGNP3      414 bp    RNA             ROD       07-MAY-1992
 DEFINITION  Mouse mRNA for idiotypic anti-NP IgG(1) heavy chain V-D-J
             (hybridoma P.5.40.1/group VI)
 ACCESSION   X02564 M12745
 KEYWORDS    gamma-immunoglobulin; Ig D-segment; Ig heavy chain; immunoglobulin;
             joining region; signal peptide; variable region.
 SOURCE      mouse
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  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Boersch-Supan,M.E., Agarwal,S., White-Scharf,M.E. and
            Imanishi-Kari,T.
  TITLE     Heavy chain variable region: Multiple gene segments encode
            anti-4-(hydroxy-3-nitrophenyl)acetyl idiotypic antibodies
  JOURNAL   J. Exp. Med. 161, 1272-1292 (1985)
  STANDARD  full automatic
COMMENT     *source: strain=C57 BL/6;

            Serological analysis of hybridomaproteins resulting from the immune
            response to the hapten NP reveals NP(a) idiotypes expressed by
            Balb/C mice and NP(b) idiotypes expressed by C57 BL/6 mice. The
            NP(b) family of antibodies consists of 6 subgroups (I-VI) with I-IV
            sharing more determinants than V and VI which appear quite
            distinct.
FEATURES             Location/Qualifiers
     sig_peptide     1..57
     mat_peptide     join(58..351,352..371,372..414)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
     misc_feature    58..351
                     /note="variable region"
     misc_feature    148..162
                     /note="CDR I"
     misc_feature    205..255
                     /note="CDR II"
     misc_feature    352..371
                     /note="D-region (aa 99-105)"
     misc_feature    372..>414
                     /note="J-region (aa 106-119)"
     CDS             join(1..351,352..371,372..414)
                     /product="idiotypic anti-NP IgG(1) heavy chain V-D-J"
                     /codon_start=1
                     /translation="MKFSWVMFFLMAVVTGVNSEVQLQQSVAELVRPGASVKLSCTAS
                     GFNIKNTYMHWVKQRPEQGLEWIGRIDPANGSTKYAPKFQIKATITADTSSNTAYLQL
                     SSLTSEDTAIYYCARYYYESSLFAYWGQGTLVTVSA"
BASE COUNT      102 a    101 c    111 g    100 t
ORIGIN

Initial Score    =    272  Optimized Score  =    308  Significance = 18.14
Residue Identity =    87%  Matches          =    315  Mismatches   =    37
Gaps             =     10  Conservative Substitutions               =     0

                                                    X       10        20
                                                    GTCAAACTGCAGCAGTCTGGGG
                                                    ||  | |||||||||||||| ||
   GCTGGGTCATGTTCTTCCTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGTGG
           20        30        40        50        60        70        80

         30        40        50        60        70        80        90
   CAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCT
   |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
   CAGAGCTTGTGAGGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAAACACCT
         90       100       110       120       130       140       150

      100       110       120       130       140       150       160
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
   ATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTA
      160       170       180       190       200       210       220

    170       180       190       200       210       220       230
   ATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGC
    |||||| |||| |||||||||||| |||||||||||| ||||| ||||| |||||||||||||||  |
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GTACTAAGTATGCCCCGAAGTTCCAGATCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACC
 230       240       250       260       270       280       290

240       250       260       270       280       290       300       310
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGTGCAGACGGAATGTGGGTATCAACGG
||||||||||||||||||||||||||||||||| |||| ||||||||    || ||     || | |||
TGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCATCTATTACTGTGC--TAGGTAT-----TA-CTACGA
300       310       320       330       340       350       360

         320       330       340       350       360
GA-TATGCTCTGGACTT-CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
|| ||  || |   ||| ||||||||||||||   |||||| |||||  ||
GAGTAGCCTGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA
     370       380       390       400       410   X
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13. US-07-977-702-1 (1-360)
    MMIGG1HCV M.musculus rearranged mRNA for anti-cytochrome c i

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LOCUS       MMIGG1HCV     351 bp    RNA             ROD       21-NOV-1991
DEFINITION  M.musculus rearranged mRNA for anti-cytochrome c immunoglobulin G1
            (IgG1) heavy chain variable region
ACCESSION   X60683
KEYWORDS    Anti-cytochrome c immunoglobulin G1; E8 variable heavy chain;
            E8 variable heavy chain D region; E8 variable heavy chain J region;
            E8 variable heavy chain V region; IgG1.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Mylvaganam,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-1991) S.E. Mylvaganam, Dept of Mol Biology, MB4,
            The Scripps Research Inst 10666 N. Torrey Pines Rd, La Jolla, CA
            92307, USA
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 351)
  AUTHORS   Mylvaganam,S.E., Paterson,Y., Kaiser,K., Bowdish,K. and
            Getzoff,E.D.
  TITLE     Biochemical Implications from the Variable Gene Sequences of an
            Anti-cytochrome c Antibody and Crystallographic Characterization of
            its Antigen-binding Fragment in Free and Antigen-complexed Forms
  JOURNAL   J. Mol. Biol. 221, 455-462 (1991)
  STANDARD  full automatic
COMMENT     *source: strain=BAKB/c;
            *source: cell_type=myeloma;
            *source: cell_line=CA4-1;

            E8 is a monoclonal antibody of the anti-cytochrome c immunoglobulin
            G1 (IgG1) that binds horse cytochrome c. E8 variable light chain -
            X60684
            E8 variable heavy chain - X60683.
FEATURES             Location/Qualifiers
     misc_feature    1..282
                     /note="heavy variable region"
     misc_feature    91..105
                     /note="first hyper-variable region"
     misc_feature    148..198
                     /note="second hyper-variable region"
     misc_feature    295..318
                     /note="third hyper-variable region"
     misc_feature    283..315
                     /note="D region"
     misc_feature    316..352
                     /note="J region"
```

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     CDS             <1..>351
                     /product="E8 variable heavy chain"
                     /codon_start=1
                     /translation="EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKG
                     LEWIGRIDPASGNTKYDPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCAGYDYG
                     NFDYWGQGTTLTVSS"
 BASE COUNT       92 a     92 c     91 g     76 t
 ORIGIN

Initial Score    =    271  Optimized Score  =    316  Significance = 18.07
Residue Identity =    89%  Matches          =    323  Mismatches   =    25
Gaps             =     12  Conservative Substitutions              =     0

      X       10        20        30        40        50        60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GAGGTTCAGCTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      X    10        20        30        40        50        60        70

  70        80        90       100       110       120       130       140
   TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
   |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
   TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAAAAGGGCCTGGAGTGGATT
        80        90       100       110       120       130       140

       150       160       170       180       190       200       210
   GGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCG
   |||||||||||||||||||||||  |||||||||||||||||||||||||| |||||||||||| |||||
   GGAAGGATTGATCCTGCGAGTGGTAATACTAAATATGACCCGAAGTTCCAGGACAAGGCCACTATAACAGCA
      150       160       170       180       190       200       210

      220       230       240       250       260       270       280
   GACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGT
   ||||| ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||| ||||||
   GACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGT
    220       230       240       250       260       270       280

     290       300       310       320       330       340       350
   GCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCC
   || |  | |||     ||  |||| |    || | |||| |||||||||||| |||||  |||| ||||||
   GCTG--GTTATG-----AT-TACGGCA---ACTTT-GACTACTGGGGCCAAGGCACCACTCTCACAGTCTCC
  290             300           310       320       330       340

     X
    TCA
    |||
    TCA
   350


14. US-07-977-702-1 (1-360)
    MUSIGMU4G    Mouse monoclonal antiidiotypic antibody IgM VDJ-re

 LOCUS       MUSIGMU4G     354 bp ss-mRNA            ROD       16-JUL-1992
 DEFINITION  Mouse monoclonal antiidiotypic antibody IgM VDJ-region mRNA.
 ACCESSION   M83722
 KEYWORDS    diversity region; immunoglobulin heavy chain;
             immunoglobulin mu-chain; joining region;
             monoclonal antiidiotypic antibody; variable region.
 SOURCE      Mus musculus hybridoma cDNA to mRNA.
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
             Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 354)
   AUTHORS   Taub,R., Hsu,J.-C., Garsky,V.M., Hill,B.L., Erlanger,B.F. and
             Kohn,L.D.
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  TITLE     Peptide sequences from the hypervariable regions of two monoclonal
            anti-idiotypic antibodies against the thyrotropin (TSH) receptor
            are similar to TSH and inhibit TSH-incresed cAMP production in
            FRTL-5 thyroid cells
  JOURNAL   J. Biol. Chem. 267, 5977-5984 (1992)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     CDS             1..348
                     /gene="IgM"
                     /partial
                     /product="immunoglobulin mu-chain"
                     /codon_start=1
                     /translation="EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQG
                     LEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAFYDYG
                     GHNWGQGTLVTVSA"
BASE COUNT       91 a     87 c     98 g     78 t
ORIGIN

Initial Score    =    271  Optimized Score  =    307  Significance = 18.07
Residue Identity =    87%  Matches          =    314  Mismatches   =    31
Gaps             =     15  Conservative Substitutions               =     0

      X       10        20        30        40        50        60
      GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GAGGTTCAGCTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCT
      X    10        20        30        40        50        60        70

   70        80        90       100       110       120       130       140
    TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATT
          80        90       100       110       120       130       140

         150       160       170       180       190       200       210
    GGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCGAAGTTCCAGGTCAAGGCCACTATTACAGCG
    |||||||||||||||||| |||  |||||||||||||||||||||||||| |||||||||||| |||||
    GGAAGGATTGATCCTGCGAATGGTAATACTAAATATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCA
       150       160       170       180       190       200       210

        220       230       240       250       260       270       280
    GACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTACTACTGT
    ||||| ||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||| ||||||
    GACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGT
     220       230       240       250       260       270       280

      290       300       310       320       330       340       350
    GCAGACGGAATGTGGGTATCAACGGGATATGCTCTGGACTTCTGGGGCCAAGGGACCACGGTCACCGTCTCC
    |    |    | ||  ||   | || |||        ||   |||||||||||||   |||||| |||||
    G----CTTTTTATGATTACGGAGGGCATA--------AC---TGGGGCCAAGGGACTCTGGTCACTGTCTCT
       290       300       310                 320       330       340

      X
    TCA
     ||
    GCAGAGAGT
      350



15. US-07-977-702-1 (1-360)
    MUSIGHBB     Mouse Ig active mu-chain VDJ-region mRNA from hybr

 LOCUS       MUSIGHBB      390 bp ss-mRNA            ROD       30-JUN-1987
 DEFINITION  Mouse Ig active mu-chain VDJ-region mRNA from hybridoma 87.92.6.
 ACCESSION   M13832
 KEYWORDS    constant region; diversity region; immunoglobulin heavy chain;
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            Immunoglobulin mu-chain; joining region; processed gene;
            variable region.
SOURCE      Mouse (Balb/c) hybridoma 87.92.6 (mu,kappa), cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 390)
  AUTHORS   Bruck,C., Co,M.S., Slaoui,M., Gaulton,G.N., Smith,T., Fields,B.N.,
            Mullins,J.I. and Greene,M.I.
  TITLE     Nucleic acid sequence of an internal image-bearing monoclonal
            anti-idiotype and its comparison to the sequence of the external
            antigen
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 83, 6578-6582 (1986)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     sig_peptide     <1..30
                     /codon_start=1
                     /note="Immunoglobulin mu-chain signal peptide"
     mat_peptide     31..>390
                     /codon_start=1
                     /note="Immunoglobulin mu-chain"
     misc_recomb     327..328
                     /note="V-region end/D-region start"
     misc_recomb     342..343
                     /note="D-region end/J-region start"
     CDS             <1..>390
                     /note="Immunoglobulin mu-chain precursor"
                     /codon_start=1
                     /translation="LMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYM
                     HWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTA
                     VYYCARGGLRRGYAMDYWGQGTSVTVSS"
BASE COUNT      100 a     96 c    111 g     83 t
ORIGIN      44 bp upstream of PstI site; chromosome 12.

Initial Score    =    271  Optimized Score  =    326  Significance = 18.07
Residue Identity =    91%  Matches          =    330  Mismatches   =    25
Gaps             =      7  Conservative Substitutions              =     0

                                  X       10        20        30
                                  GTCAAACTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCA
                                  ||  | ||||||||||||||||||||||||||||||||||
   CTGATGGCAGTGGTTACAGGGGTCAATTCAGAGGTTCAGCTGCAGCAGTCTGGGGCAGAGCTTGTGAAGCCA
           10        20        30   X    40        50        60        70

  40        50        60        70        80        90       100       110
   GGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   GGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTATATGCACTGGGTGAAG
         80        90       100       110       120       130       140

         120       130       140       150       160       170       180
   CAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAGTGGCGATACTAAATATGACCCG
   ||||||||||||||||||||||||||||||||||||||||||||||||| |||  ||||||||||||||||
   CAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGTAATACTAAATATGACCCG
      150       160       170       180       190       200       210

        190       200       210       220       230       240       250
   AAGTTCCAGGTCAAGGCCACTATTACAGCGGACACGTCCTCCAACACAGCCTGGCTGCAGCTCAGCAGCCTG
   |||||||||| |||||||||||| ||||| ||||| ||||||||||||||||  ||||||||||||||||||
   AAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTCCAACACAGCCTACCTGCAGCTCAGCAGCCTG
    220       230       240       250       260       270       280

     260       270       280       290       300       310       320
   ACATCTGAGGACACTGCCGTCTACTACTGTGC-AGACGGAATGTGGGTATCAAC-GGGATATGCTCTGGACT
   |||||||||||||||||||||| |||||||| ||| ||     || |  | || ||| |||||| ||||||
   ACATCTGAGGACACTGCCGTCTATTACTGTGCTAGAGGG-----GGATTACGACGGGGGTATGCTATGGACT
```

```
290        300        310        320        330        340        350

      330        340        350         X
    TCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
     ||||||  |||||  |||  |  ||||||||||||||||
    ACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA
      360        370        380        390
```

Seq. 2

```
> 0 <
0| |0  IntelliGenetics
> 0 <

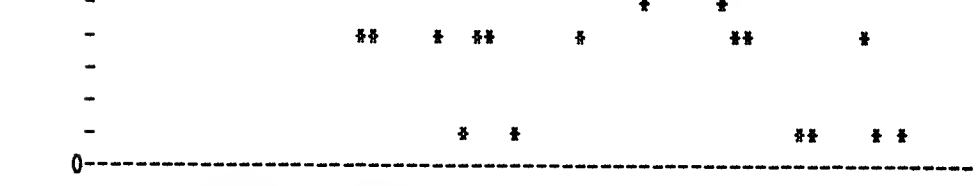
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-977-702-2-ngs.res made by shears on Tue 15 Jun 93 11:11:14-PDT.


Query sequence being compared:US-07-977-702-2 (1-318)
Number of sequences searched:                25646
Number of scores above cutoff:                4637

     Results of the initial comparison of US-07-977-702-2 (1-318) with:
   Data bank : N-GeneSeq 10, all entries

 10000-*
      -
N     -
U 5000-
M     - *
B     -
E     -  **
R     -    **
      -      *
0     -       *
F 1000-        *
      -
S     -
E  500*
Q     -         *
U     -          *
E     -           *
N     -
C     -            *
E     -
S  100-
      -             *
      -
     50-               *
      -
      -              *
      -                *
      -
      -                  **                    *
      -                                *  *        *
     10-                  *                 *     *     *            *
      -                                    *
      -                        * *             **
      5-                           *   *           ** *    *
      -
```



PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	32
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		
Initial scores to save	40	Alignments to save	15
Optimized scores to save	0	Display context	50

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	17	14	12.85

Times:	CPU	Total Elapsed
	00:03:01.00	00:06:12.00

Number of residues: 14371384
Number of sequences searched: 25646
Number of scores above cutoff: 4637

Cut-off raised to 8.
Cut-off raised to 15.
Cut-off raised to 22.
Cut-off raised to 26.
Cut-off raised to 29.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 19 standard deviations above mean ****					
1. Q04265	Encodes Colon Cancer monoclon	381	263	265	19.14	0
	**** 18 standard deviations above mean ****					
2. Q28254	VL FRP5.	407	260	263	18.91	0
3. Q28653	DNA encoding 1E6 kappa light	327	257	260	18.68	0
4. Q28262	Fv(FRP5)-ETA fusion gene.	2011	257	260	18.68	0
5. Q28257	Fv(FRP5)-phoA recombinant ant	2233	257	260	18.68	0
6. Q04592	Sequence encoding region of h	324	256	257	18.60	0
7. N90813	DNA encoding light chain vari	324	256	257	18.60	0
8. Q27132	Light chain variable region c	387	256	257	18.60	0
9. Q28256	Fv heavy chain/light chain va	748	256	259	18.60	0
10. Q05557	Sequence encoding variable re	411	255	259	18.52	0
11. N40022	cDNA insert of pK17G4 encodin	882	252	254	18.29	0
12. Q04264	Encodes Colon Cancer monoclon	685	250	253	18.13	0

13.	N40023	mRNA encoding kappa anti-CarC	882	249	253	18.06	0
		**** 16 standard deviations above mean ****					
14.	G25592	Encodes 4D5 Fab IgG antibody	2178	234	237	16.89	0
15.	G28747	Anti-CEA specific light chain	387	227	257	16.34	0
		**** 15 standard deviations above mean ****					
16.	N81636	Anti-pseudomonas aeruginosa h	324	216	219	15.49	0
17.	N81638	Anti-pseudomonas aeruginosa h	671	216	220	15.49	0
18.	G10946	Feline immunoglobulin kappa c	618	214	221	15.33	0
19.	G11191	V region gene JP2gL411 from a	618	214	221	15.33	0
20.	G04654	Plasmid pBT111 encoding antib	5238	213	214	15.25	0
21.	G29150	WN1 222-5 antibody Light chai	322	210	215	15.02	0
		**** 14 standard deviations above mean ****					
22.	G12017	Sequence encoding mouse MAb 1	402	208	216	14.86	0
23.	G12061	Sequence encoding light (kapp	402	208	216	14.86	0
24.	G29151	WN1 58-9 antibody Light chain	321	204	213	14.55	0
25.	G15114	IL-2 chimeric antibody light	432	204	211	14.55	0
26.	G23566	Rat CD4 antibody light chain	620	204	209	14.55	0
27.	G05556	Sequence encoding variable re	419	200	210	14.24	0
28.	N90672	DNA sequence encoding uproces	420	200	208	14.24	0
29.	G15113	IL-2 chimeric antibody light	432	200	207	14.24	0
30.	G08608	ME4 Light Chain V Region (mou	444	200	208	14.24	0
31.	G12633	CD4-specific CDR-grafted ligh	754	200	208	14.24	0
32.	N90500	Light chain antibody variable	608	198	206	14.09	0
33.	G23567	Reshaped CAMPATH-1 antibody l	748	198	206	14.09	0
34.	G20381	Sequence encoding the shorten	819	198	208	14.09	0
35.	G23568	Reshaped CD4 antibody light c	748	197	205	14.01	0
36.	N90300	Insert coding for light chain	1395	197	207	14.01	0
		**** 13 standard deviations above mean ****					
37.	G11848	Human anti-placental alkaline	324	194	204	13.77	0
38.	G21097	FabD1.3 in pUC19.	1526	194	203	13.77	0
39.	G11846	Anti-placental alkaline phosp	324	193	203	13.70	0
40.	N30165	Sequence encoding the leader,	450	192	199	13.62	0

1. US-07-977-702-2 (1-318)
   G04265 Encodes Colon Cancer monoclonal antibody CC92 ligh

ID G04265 standard; DNA; 381 BP.
AC G04265;
DT 13-SEP-1990 (first entry)
DE Encodes Colon Cancer monoclonal antibody CC92 light chain variable region
KW chimeric antibodies; TAG72; light chain variable region;
KW heavy chain variable region; ss
OS synthetic.
PN EP-365997-A.
PD 02-MAY-1990.
PF 18-OCT-1989; 119361.
PR 19-OCT-1988;US-259943.
PA (DOWC) Dow Chemical Co.
PI Mezes P, Gourlie B, Rixon M;
DR WPI; 90-133521/18.
DR P-PSDB; R04388.
PT Chimeric antibodies against TAG72 and conjugate to provide imaging
PT markers and therapeutic tools
PS Disclosure; pp; English.
CC The polypeptide encoded by this sequence forms part of a chimera. The
CC other components are a heavy chain variable region and human-derived
CC constant light and heavy chain regions. The variable regions have
CC high affinity for TAG72. The constant regions reduce the side-effects
CC when administered to human patients because they are of human origin.
CC See also G04258-64 and G04266-9.
SQ Sequence 381 BP; 90 A; 90 C; 97 G; 104 T;

Initial Score	=	263	Optimized Score	=	265	Significance	= 19.14
Residue Identity	=	83%	Matches	=	266	Mismatches	= 52
Gaps	=	1	Conservative Substitutions			=	0

```
                                                    X        10        20
                                                    AG-TATTGTGATGACCCAGACT
                                                    ||  ||||||||||||||| ||
   AGATCCAGGTCCTTTGTATTCGTGTTTCTCTGGTTGTCTGGTGTTGACGGAGACATTGTGATGACCCAGTCT
    10        20        30        40        50        60        70

          30        40        50        60        70        80        90
   CCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
   | ||||||| ||      |||| |||||||||||| | ||| ||||||||||||||||||  ||||| || |
   CACAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGAGTAGT
 80        90        100       110       120       130       140       150

     100       110       120       130       140       150       160
   GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
   | |||||  ||||  |||||||| ||||| || ||||||||| | ||||| ||||  |||||| | || ||
   GCTGTAGGGTGGTTTCAACAGAAACCAGGACAATCTCCTAAATTACTGATTTATTCGGCATCCTACCGGTAT
         160       170       180       190       200       210       220

     170       180       190       200       210       220       230
   ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAG
   |||||||||||||||||||||||||||||||| | ||||||||||||||||||||| || |||||||
   ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTCGGACGGATTTCACTTTCACCATCACCAGTGTGCAG
      230       240       250       260       270       280       290

   240       250       260       270       280       290       300
   GCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAG
   |||||||||||||||||||| |||||||||  |||||||   ||||  ||||||||| |  |||||||||
   GCTGAAGACCTGGCAGTTTATTACTGTCAGCAACATTATAGTAGTCCGCTCACGTTCGGTGCTGGGACCAAG
     300       310       320       330       340       350       360

  310       X
    CTGGAGATC
    |||||| |
    CTGGAGCTGAAACT
    370     X 380
```

2. US-07-977-702-2 (1-318)
   Q28254 VL FRP5.

```
 ID   Q28254 standard; DNA; 407 BP.
 AC   Q28254;
 DT   11-FEB-1993  (first entry)
 DE   VL FRP5.
 KW   Minigene; pMZ18/1; monoclonal antibody; kappa; light chain;
 KW   variable region; pWW31; ss.
 OS   Mus musculus.
 PN   EP-502812-A.
 PD   09-SEP-1992.
 PF   27-JAN-1992; 810056.
 PR   05-FEB-1991; EP-810079.
 PA   (CIBA ) CIBA GEIGY AG.
 PI   Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
 PI   Zwickl M;
 DR   WPI; 92-302096/37.
 PT   Recombinant antibodies directed to growth factor receptor C-erbB-2 -
 PT   for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
 PT   or ovarian tumours
 PS   Disclosure; Page 29; 67pp; English.
 CC   The sequence given a portion of the plasmid pMZ18/1 and encodes the
 CC   kappa light chain variable (V) domain of the monoclonal antibody FRP5.
 CC   The V-region was excised from this plasmid and cloned into plasmid
 CC   pWW31 which was used in the construction of a recombinant antibody
 CC   which is directed to the extracellular domain of the growth factor
 CC   c-erbB-2.
```

```
 Sq   Sequence   407 BP;    101 A;    107 C;    94 G;    105 T;

Initial Score    =    260  Optimized Score  =    263  Significance = 18.91
Residue Identity =    82%  Matches          =    264  Mismatches   =    54
Gaps             =      1  Conservative Substitutions              =     0

                           X        10        20        30        40
                           AG-TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGC
                           ||  ||||||||||||||| ||| ||||||||||     |||||
   TCTAGTCACTGGATGGTGGGAAGATGGAGACATTGTGATGACCCAGTCTCACAAATTCCTGTCCACTTCAGT
           10        20        30        40        50        60        70

       50        60        70        80        90       100       110
   AGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAA
   ||||||||||||  | ||| ||||||||||||||||||  ||||  ||||| ||| || ||||| ||||||||
   AGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATGCTGTTGCCTGGTATCAACAGAA
         80        90       100       110       120       130       140

    120       130       140       150       160       170       180
   GCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCAC
    |||||  ||  ||||||||||| |||||  ||  |  ||||||   ||  ||||||||||||||  |||||||||
   ACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACACTGGAGTCCCTTCTCGCTTCAC
      150       160       170       180       190       200       210

  190       200       210       220       230       240       250       260
   TGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTT
   |||||||||  |  ||||  ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
   TGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTT
    220       230       240       250       260       270       280

          270       280       290       300       310       X
   CTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGATC
   |||||||||  |||  |  |  ||||  |  |||||||||   ||||||  ||  ||||  ||
   CTGTCAGCAACATTTTCGTACTCCATTCACGTTCGGCTCGGGGACAAAATTGGAAATAAAACGGGCTGATGC
  290       300       310       320       330       340     X 350       360

   TGCACCAACTGTATCCATCTTCCCACCATCCAGTGA
          370       380       390
```

3. US-07-977-702-2 (1-318)
   Q28653 DNA encoding 1E6 kappa light chain variable region

```
 ID   Q28653 standard; DNA; 327 BP.
 AC   Q28653;
 DT   17-FEB-1993  (first entry)
 DE   DNA encoding 1E6 kappa light chain variable region.
 KW   Chimeric; heavy chain; variable region; monoclonal antibody;
 KW   lymphocyte function associated antigen-3; LFA-3; inflammation;
 KW   autoimmune disease; immunomodulation; systemic lupus erythematosus;
 KW   rheumatoid arthritis; thyroiditis; ss.
 OS   Homo sapiens.
 PN   EP-503646-A.
 PD   16-SEP-1992.
 PF   12-MAR-1992; 104318.
 PR   12-MAR-1991; US-667975.
 PA   (BIOJ ) BIOGEN INC.
 PI   Chisholm PL, Sato VL, Wallner BP;
 DR   WPI; 92-309758/38.
 DR   P-PSDB; R27144.
 PT   Monoclonal antibodies active against lymphocyte function
 PT   associated antigen-3 - for treating inflammation and auto:immune
 PT   diseases, and for detecting LFA-3 protein in a sample
 PS   Claim 16; Page 14; 30pp; English.
 CC   DNA sequences obtd. from the hybridoma cell line 1E6-2C12 (ATCC HB
 CC   10693) encoding the light and heavy chain regions of 1E6 were
```

CC amplified for cloning and sequencing using PCR. The PCR primers for
CC the light chain variable region were MKVP7 and 360-41, and the heavy
CC chain primers were VH01 and VH02. The PCR prods. were
CC electrophoresed on agarose gel and the DNA excised and inserted into
CC plasmids. The light and heavy chain regions may be used to
CC construct a monoclonal antibody active against LFA-3 which blocks
CC adhesion of LFA-3 expressing cells to lymphocytes. The antibody may
CC be used in the treatment and diagnosis of acute and chronic
CC inflammation, autoimmune diseases and for immunomodulation including
CC systemic lupus erythematosus, rheumatoid arthritis and thyroiditis.
CC See also 028654-8.
SQ Sequence 327 BP; 89 A; 82 C; 83 G; 73 T;

Initial Score = 257 Optimized Score = 260 Significance = 18.68
Residue Identity = 81% Matches = 260 Mismatches = 58
Gaps = 0 Conservative Substitutions = 0

```
X       10        20        30        40        50        60        70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
|  ||||| ||||||||  |||||||||| | ||    | |||| |||||| ||||| ||| | |||||||||
AACATTGTAATGACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGAGAGGGTCACCTTGACCTGCAAG
X       10        20        30        40        50        60        70

      80        90       100       110       120       130       140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
||||||  |||  ||||  || | ||||  | |||||  |||||||| |||| |||||||||||||||||  |||
GCCAGTGAGAATGTGGTTACTTATGTTTCCTGGTATCAACAGAAACCAGAGCAGTCTCCTAAACTGCTCATA
      80        90       100       110       120       130       140

   150       160       170       180       190       200       210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
||    ||||||||  ||  ||||||||  |||||  ||||||||||  ||||||||||  ||  ||  |||||||||
TACGGGGCATCCAACCGGTACACTGGGGTCCCCGATCGCTTCACAGGCAGTGGATCTGCAACAGATTTCACT
   150       160       170       180       190       200       210

 220       230       240       250       260       270       280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
 | ||||||||||  ||||||||||||||||||  ||||  ||||   ||||  |||  ||||  |||||||
CTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACTGTGGACAGGGTTACAGCTATCCGTAC
 220       230       240       250       260       270       280

290       300       310       X
ACGTTCGGAGGGGGGACCAAGCTGGAGATC
|||||||||||||||||||||||||||  ||
ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCT
290       300       310       320
```

4. US-07-977-702-2 (1-318)
   028262 Fv(FRP5)-ETA fusion gene.

ID 028262 standard; DNA; 2011 BP.
AC 028262;
DT 11-FEB-1993 (first entry)
DE Fv(FRP5)-ETA fusion gene.
KW Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2;
KW variable region; ETA; ss.
OS Pseudomonas aeruginosa PAK.
FH Key Location/Qualifiers
FT sig_peptide 1..63
FT /*tag= a
FT /label= ompA_signal_peptide
FT misc_RNA 64..87
FT /*tag= b
FT /note= "FLAG peptide and enterokinase cleavage site"
FT misc_RNA 97..453

FT /*tag= c
FT /label= FRP5_heavy_chain_variable_domain
FT misc_RNA 454..498
FT /*tag= a
FT /label= Linker
FT misc_RNA 499..822
FT /*tag= a
FT /label= FRP5_light_chain_variable_domain
FT CDS 826..1911
FT /*tag= a
FT /label= ETA_1574-1747
FT 3'clip 1912..2012
FT /*tag= a
FT /label= ETA_3'_non-coding_region
PN EP-502812-A.
PD 09-SEP-1992.
PF 27-JAN-1992; 810056.
PR 05-FEB-1991; EP-810079.
PA (CIBA) CIBA GEIGY AG.
PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
PI Zwickl M;
DR WPI; 92-302096/37.
DR P-PSDB; R26982.
PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
PT or ovarian tumours
PS Disclosure; Page 47-52; 67pp; English.
CC The sequences given in Q28261-3 encode part of the exotoxin A (ETA)
CC sequence corresponding to positions 1574-1747 of the full exotoxin A
CC sequence. These sequences were used in the construction of
CC Fv(FRP5)-ETA fusion genes. The ETA sequence was used as a marker gene
CC so that E. coli transformed with the fusion gene could be identified.
CC The fusion genes were expressed in E. coli and the antibody was
CC extracted. This recombinant antibody can be used for the qualitative
CC and quantitative determination of c-erbB-2. This can be used for
CC monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
SQ Sequence 2011 BP; 383 A; 653 C; 620 G; 355 T;

Initial Score = 257 Optimized Score = 260 Significance = 18.68
Residue Identity = 81% Matches = 260 Mismatches = 58
Gaps = 0 Conservative Substitutions = 0

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                                                X       10        20
                                                AGTATTGTGATGACCCAGACTC
                                                  ||   | ||||||| |||
    CCTCTGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTC
  450       460       470       480       490       500       510       520

        30        40        50        60        70        80        90
    CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
     ||||||||||     ||||| ||||||||||||| | ||| ||||||||||||||||||  ||||  |||||
    ACAAATTCCTGTCCACTTCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATG
          530       540       550       560       570       580       590

       100       110       120       130       140       150       160
    ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
     ||| || ||||| |||||||| ||||| || |||||||||||| ||||| || |  ||||||   || ||||
    CTGTTGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACA
        600       610       620       630       640       650       660

     170       180       190       200       210       220       230
    CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
    ||||||||||| |||||||||||||||||| | |||| |||||||||||||||||||||||| ||||||||
    CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCAGTGTGCAGG
       670       680       690       700       710       720       730
```

```
240       250       260       270       280       290       300       310
CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
||||||||||||||||||||||||||||||  ||| | |  |||| | |||||||||   |||||| ||
CTGAAGACCTGGCAGTTTATTTCTGTCAGCAACATTTTCGTACTCCATTCACGTTCGGCTCGGGGACAAAAT
 740       750       760       770       780       790       800

        X
TGGAGATC
||||||||
TGGAGATCAAAGCTCTAGAGGGCGGCAGCCTGGCCGCGCTGACCGCGCACCAGGCCTG
810     X 820       830       840       850       860
```

5. US-07-977-702-2 (1-318)
   Q28257 Fv(FRP5)-phoA recombinant antibody.

ID Q28257 standard; DNA; 2233 BP.
AC Q28257;
DT 11-FEB-1993 (first entry)
DE Fv(FRP5)-phoA recombinant antibody.
KW Monoclonal antibody; light chain; heavy chain; tumour; phoA;
KW variable region; alkaline phosphatase; c-erbB-2; ss
OS Synthetic.
FH Key   Location/Qualifiers
FT CDS   23..2158
FT /*tag= a
FT sig_peptide   23..85
FT /*tag= b
FT /label= ompA_signal_peptide
FT misc_RNA   89..445
FT /*tag= c
FT /label= FRP5_heavy_chain_variable_domain
FT misc_RNA   446..490
FT /*tag= d
FT /label= Linker
FT misc_RNA   491..814
FT /*tag= e
FT /label= FRP5_light_chain_variable_domain
FT mat_peptide   815..2155
FT /*tag= f
FT /label= phoA_coding_region
PN EP-502812-A.
PD 09-SEP-1992.
PF 27-JAN-1992; 810056.
PR 05-FEB-1991; EP-810079.
PA (CIBA) CIBA GEIGY AG.
PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
PI Zwickl M;
DR WPI; 92-302096/37.
DR P-PSDB; R26980.
PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
PT or ovarian tumours
PS Disclosure; Page 34-40; 67pp; English.
CC The sequence given encodes the single chain recombinant antibody
CC desiganted Fv(FRP5)-phoA. The alkaline phosphatase gene (phoA) was
CC used as a marker gene so that E. coli transformed with the fusion gene
CC could be identified. The fusion gene was expressed in E. coli and the
CC antibody was extracted. This recombinant antibody can be used for the
CC qualitative and quantitative determination of c-erbB-2. This can be
CC used for monitoring or in-vivo localisation of tumours overexpressing
CC c-erbB-2.
SQ Sequence 2233 BP; 566 A; 573 C; 606 G; 488 T;

Initial Score   = 257 Optimized Score = 260 Significance = 18.68
Residue Identity = 81% Matches   = 260 Mismatches   = 58

```
Gaps            =      0  Conservative Substitutions              =      0

                                                        X       10        20
                                                        AGTATTGTGATGACCCAGACTC
                                                          ||   | ||||||||  |||
    CCTCTGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTC
           450       460       470       480       490       500       510

          30        40        50        60        70        80        90
    CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
     ||||||||||     ||||| ||||||||||||  | ||| ||||||||||||||||||  ||||  |||||
    ACAAATTCCTGTCCACTTCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATG
         520       530       540       550       560       570       580

       100       110       120       130       140       150       160
    ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
     ||| || ||||| ||||||||  ||||| || ||||||||||| ||||| || |  ||||||   || ||||
    CTGTTGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACA
       590       600       610       620       630       640       650

     170       180       190       200       210       220       230
    CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
    ||||||||||  |||||||||||||||||| | |||| |||||||||||||||||||||||| ||||||||
    CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCAGTGTGCAGG
     660       670       680       690       700       710       720

   240       250       260       270       280       290       300       310
    CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
    ||||||||||||||||||||||||||||||  ||| | |  |||| | |||||||||  ||||||  ||
    CTGAAGACCTGGCAGTTTATTTCTGTCAGCAACATTTTCGTACTCCATTCACGTTCGGCTCGGGGACAAAAT
  730       740       750       760       770       780       790       800

          X
    TGGAGATC
    ||||||||
    TGGAGATCAAAGCTCTAGAGCCTGTTCTGGAAAACCGGGCTGCTCAGGGCGATATTAC
          810       820       830       840       850
```

6. US-07-977-702-2 (1-318)
   Q04592 Sequence encoding region of human carcinoembrionic

```
ID   Q04592 standard; DNA; 324 BP.
AC   Q04592;
DT   28-SEP-1990  (first entry)
DE   Sequence encoding region of human carcinoembrionic light chain
DE   antigen (CEA).
KW   Carcinoembryonic antigen; CEA; Chelate-specific antigen; CHA;
KW   tumor; cancer; serum sickness.
OS   Homo sapiens.
PN   EP-369566-A.
PD   23-MAY-1990.
PF   8-MAR-1989; 302313.
PR   17-NOV-1988; US-274105; EP-302313.
PA   (HYBR-) Hybritech Inc.
PI   Johnson MJ, Phelps JL;
DR   WPI; 90-157695/21.
DR   P-PSDB; R04936.
PT   Bifunctional chimeric antibodies -
PT   having variable regions which recognise different antigens and
PT   metal chelates and human constant regions.
PS   Claim 2; Page 24; 40pp; English.
CC   Gene encodes portion of CEA light chain antigen, useful in
CC   generating chimeric monoclonal antibody binding to CEA at a tumour
CC   site and a metal chelate bonded to say a toxin or other drug.
SQ   Sequence   324 BP;   85 A;   83 C;   77 G;   79 T;
```

```
Initial Score    =    256  Optimized Score  =    257  Significance = 18.60
Residue Identity =    80%  Matches         =    257  Mismatches   =    61
Gaps             =      0  Conservative Substitutions             =     0

    X       10        20        30        40        50        60        70
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
       ||||||||||||||| |||  |||||| ||      |||| |||||||||||| | ||| |||||||||
    GACATTGTGATGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
    |||||||||| |||   || || ||| || ||||| |||||||| ||||||||||||||||||   |||||
    GCCAGTCAGAATGTTCGTACTGCTGTTGCCTGGTATCAACAGAAACCAGGGCAGTCTCCTAAAGCACTGATT
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
    || |  |||||||| || ||||||||||||||||||||||||||| |||||||||| |||||| |||||||||
    TACTTGGCATCCAACCGGTACACTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACT
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
     |||||||  | || ||||||  |||||||||||||||| |||||||||| |||  |||  |  | ||||  |
    CTCACCATTACCAATGTGCAATCTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCCGCTC
     220       230       240       250       260       270       280

   290       300       310       X
    ACGTTCGGAGGGGGGACCAAGCTGGAGATC
    |||||||| |  |||||||||||||||| |
    ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAACGG
   290       300       310       320
```

7. US-07-977-702-2 (1-318)
   N90813 DNA encoding light chain variable region against c

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ID   N90813 standard; cDNA; 324 BP.
AC   N90813;
DT   24-JAN-1990. (first entry)
DE   DNA encoding light chain variable region against carcinoembryonic antigen
KW   Carcinoembyonic antigen; immunogen; tumour; chimeric antibody.
OS   Murine (mouse) hybridoma CEM 231.6,7 (ATCC HB 9620).
FH   Key             Location/Qualifiers
FT   CDS             1..324
FT   /*tag=  a
PN   EP-332424-A.
PD   13-SEP-1989.
PF   08-MAR-1989; 302312.
PR   09-MAR-1988; US-272577.
PA   (HYBR) Hybritech Inc.
PI   Beidler CB, Johnson MJ, Ludwig JR, Carlo DJ, David GS;
DR   WPI; 89-265635/37.
DR   P-PSDB; P91381.
PT   DNA constructs encoding light or heavy chain variable regions
PT   - chimeric monoclonal antibody, specific for human
PT   carcinoembryonic antigen, useful for diagnosis, imaging and
PT   treatment of tumours.
PS   Claim 2; page 18; 32pp; English.
CC   This region contained in a DNA construct with heavy chain variable
CC   and constant regions, light chain constant region, and 2 eukaryotic
CC   leader sequences. The chimeric monoclonal antibodies thus formed
CC   can be directed against CEA for immunoassay, and imaging and
CC   treatment of tumours, eg colorectal or breast carcinoma. The
```

CC constant regions are human-derived and so are less immunogenic
CC than entirely murine Abs.
SQ Sequence 324 BP; 85 A; 83 C; 77 G; 79 T;

Initial Score = 256 Optimized Score = 257 Significance = 18.60
Residue Identity = 80% Matches = 257 Mismatches = 61
Gaps = 0 Conservative Substitutions = 0

```
X       10        20        30        40        50        60        70
AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
   ||||||||||||||| |||  |||||| ||      |||| ||||||||||||| | ||| |||||||||
GACATTGTGATGACCCAGTCTCAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAG
X       10        20        30        40        50        60        70

      80        90       100       110       120       130       140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
||||||||||| |||   || || ||| || ||||| |||||||| ||||||||||||||||||   |||||
GCCAGTCAGAATGTTCGTACTGCTGTTGCCTGGTATCAACAGAAACCAGGGCAGTCTCCTAAAGCACTGATT
      80        90       100       110       120       130       140

   150       160       170       180       190       200       210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
|| |  |||||||| || ||||||||||||||||||||||||| |||||||||| |||||| |||||||||
TACTTGGCATCCAACCGGTACACTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACT
   150       160       170       180       190       200       210

 220       230       240       250       260       270       280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
 |||||||  | || ||||||  |||||||||||||||| |||||||||| |||  |||  |  | ||||  |
CTCACCATTACCAATGTGCAATCTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCCGCTC
 220       230       240       250       260       270       280

290       300       310       X
ACGTTCGGAGGGGGGACCAAGCTGGAGATC
|||||||| |  |||||||||||||| |
ACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAACGG
290       300       310       320
```

8. US-07-977-702-2 (1-318)
027132 Light chain variable region contg. ompA leader pep

ID 027132 standard; DNA; 387 BP.
AC 027132;
DT 21-JAN-1993 (first entry)
DE Light chain variable region contg. ompA leader peptide.
KW Heavy; antibody; Fv; CEM231.6.7; VL; ss; chelator.
OS Synthetic.
PN EP-497585-A.
PD 05-AUG-1992.
PF 30-JAN-1992; 300775.
PR 30-JAN-1991; US-647901.
PA (ANDE/) ANDERSON L D.
PA (COOK/) COOK J A.
PA (DAVI/) DAVID G S.
PA (HOCH/) HOCHSCHWENDER S M.
PA (KASH/) KASHER M S.
PA (SMIT/) SMITH M C.
PA (STEM/) STEMMER W P C.
PI Anderson LD, Cook JA, David GS, Hochschwenderder SM, Kasher MS;
PI Smith MC, Stemmer WPC;
DR WPI; 92-261005/32.
PT Immobilisation and purification of molecules - using kinetically
PT inert immobilised metal-CP-protein complex useful in assay
PT system
PS Example 5; Page 37; 88pp; English.

```
CC   Sequencing of cloned CEM231.6.7. heavy and light chain variable
CC   regions along with the His-Trp-His-His-His fusion peptide was
CC   performed by standard procedures.  This sequence shows the light
CC   chain variable sequence contg. the ompA leader peptide.
CC   See also Q27108-33.
SQ   Sequence   387 BP;    100 A;    100 C;    96 G;    91 T;

Initial Score    =    256  Optimized Score  =    257  Significance = 18.60
Residue Identity =    80%  Matches          =    257  Mismatches   =    61
Gaps             =      0  Conservative Substitutions               =     0

                                                    X       10        20
                                                    AGTATTGTGATGACCCAGACTC
                                                      ||||||||||||||| |||
    CTATCGCGATCGCAGTGGCACTGGCTGGTTTCGCCACCGTGGCGCAGGCCGACATTGTGATGACCCAGTCTC
         20        30        40        50        60   X    70        80

          30        40        50        60        70        80        90
    CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
      |||||| ||      |||| ||||||||||||| | ||| ||||||||||||||||||| |||   || ||
    AAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGAATGTTCGTACTG
       90       100       110       120       130       140       150

         100       110       120       130       140       150       160
    ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
     ||| || ||||| |||||||| ||||||||||||||||||   ||||| || |  |||||||| || ||||
    CTGTTGCCTGGTATCAACAGAAACCAGGGCAGTCTCCTAAAGCACTGATTTACTTGGCATCCAACCGGTACA
    160       170       180       190       200       210       220

     170       180       190       200       210       220       230
    CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
    ||||||||||||||||||||| |||||||||| |||||| ||||||||| ||||||| | || ||||||
    CTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTACCAATGTGCAAT
  230       240       250       260       270       280       290       300

   240       250       260       270       280       290       300       310
    CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
    ||||||||||||||| |||||||||| |||  |||  |  | ||||  ||||||||| |  ||||||||||
    CTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCCGCTCACGTTCGGTGCTGGGACCAAGC
         310       320       330       340       350       360       370

          X
    TGGAGATC
    ||||| |
    TGGAGCTGAAATAG
        380


9. US-07-977-702-2 (1-318)
   Q28256       Fv heavy chain/light chain variable domain fusion

 ID   Q28256 standard; DNA; 748 BP.
 AC   Q28256;
 DT   11-FEB-1993  (first entry)
 DE   Fv heavy chain/light chain variable domain fusion protein.
 KW   Minigene; pMZ18/1; monoclonal antibody; kappa; light chain;
 KW   variable region; pWW31; tuomour; ss.
 OS   Mus musculus.
 FH   Key             Location/Qualifiers
 FT   CDS             5..731
 FT   /*tag=  a
 FT   misc_RNA        9..365
 FT   /*tag=  b
 FT   /label= FRP5_heavy_chain_variable_domain
 FT   misc_RNA        99..113
 FT   /*tag=  c
```

FT /label= CDR1H
FT misc_RNA 156..206
FT /*tag= d
FT /label= CDR2H
FT misc_RNA 303..332
FT /*tag= e
FT /label= CDR3H
FT misc_RNA 366..410
FT /*tag= f
FT /label= Linker
FT misc_RNA 411..728
FT /*tag= g
FT /label= FRP5_light_chain_variable_domain
FT misc_RNA 480..512
FT /*tag= h
FT /label= CDR1L
FT CDS 558..578
FT /*tag= i
FT /label= CDR2L
FT misc_RNA 675..701
FT /*tag= j
FT /label= CDR3L
PN EP-502812-A.
PD 09-SEP-1992.
PF 27-JAN-1992; 810056.
PR 05-FEB-1991; EP-810079.
PA (CIBA) CIBA GEIGY AG.
PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
PI Zwickl M;
DR WPI; 92-302096/37.
DR P-PSDB; R26979.
PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
PT or ovarian tumours
PS Disclosure; Page 31-33; 67pp; English.
CC The sequence given encodes the Fv heavy chain/light chain variable
CC domain fusion protein which binds to the extracellular domain of the
CC growth factor receptor c-erbB-2. This recombinant antibody can be used
CC for the qualitative and quantitative determination of c-erbB-2. This
CC can be used for monitoring or in-vivo localisation of tumours
CC overexpressing c-erbB-2.
SQ Sequence 748 BP; 178 A; 190 C; 192 G; 188 T;

Initial Score = 256 Optimized Score = 259 Significance = 18.60
Residue Identity = 81% Matches = 259 Mismatches = 59
Gaps = 0 Conservative Substitutions = 0

```
                                                X       10        20
                                                AGTATTGTGATGACCCAGACTC
                                                  ||   | ||||||||| |||
    CCTCTGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTC
          370       380       390       400       410       420       430

         30        40        50        60        70        80        90
    CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
     ||||||||||     ||||| |||||||||||| | ||| ||||||||||||||||||  ||||  |||||
    ACAAATTCCTGTCCACTTCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGTATAATG
         440       450       460       470       480       490       500

       100       110       120       130       140       150       160
    ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
     ||| || ||||| |||||||| ||||| || |||||||||||| ||||| || |  ||||||   || ||||
    CTGTTGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTTCTGATTTACTCGGCATCCTCCCGGTACA
       510       520       530       540       550       560       570

     170       180       190       200       210       220       230
```

```
CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCACTGTGCAGG
||||||||||| |||||||||||||||||| | |||| |||||||||||||||||||||||| ||||||||
CTGGAGTCCCTTCTCGCTTCACTGGCAGTGGCTCTGGGCCGGATTTCACTTTCACCATCAGCAGTGTGCAGG
 580       590       600       610       620       630       640

240       250       260       270       280       290       300       310
CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
|||||||||||||||||||||||||||||||  ||| | |  |||| | |||||||||   |||||| ||
CTGAAGACCTGGCAGTTTATTTCTGTCAGCAACATTTTCGTACTCCATTCACGTTCGGCTCGGGGACAAAAT
650       660       670       680       690       700       710       720

        X
TGGAGATC
| ||||||
TCGAGATCTAGCTGATCAAAGCTCTAGA
        730       740
```

10. US-07-977-702-2 (1-318)
    Q05557 Sequence encoding variable region of murine AHT 54

```
 ID   Q05557 standard; DNA; 411 BP.
 AC   Q05557;
 DT   10-DEC-1990  (first entry)
 DE   Sequence encoding variable region of murine AHT 54 light chain.
 KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
 OS   Mus sp.
 FH   Key             Location/Qualifiers
 FT   CDS             58..411
 FT   /*tag=  a
 PN   EP-380068-A.
 PD   01-AUG-1990.
 PF   24-JAN-1990; 101351.
 PR   24-JAN-1989; US-301216.
 PR   04-DEC-1989; US-441702.
 PA   (MOLE-) MOLECULAR THERAPEU.
 PI   Zerler B;
 DR   WPI; 90-232892/31.
 DR   P-PSDB; R06253.
 PT   Expression vectors for producing chimeric monoclonal antibodies -
 PT   which express human constant region and non-human variable region
 PS   Disclosure; p; English.
 CC   MAbs comprising mouse CH and CL constant regions whith human
 CC   variable regions may be used to create mouse/human hybrid MAbs,
 CC   which have a longer serum half-life. Method can be used to produce
 CC   Abs against interleukin-2 receptor and tumour necrosis factor.
 SQ   Sequence   411 BP;    110 A;    94 C;    104 G;    103 T;

Initial Score    =    255  Optimized Score  =    259  Significance = 18.52
Residue Identity =    81%  Matches          =    260  Mismatches   =    58
Gaps             =      1  Conservative Substitutions               =     0

                                                    X       10        20
                                                    AG-TATTGTGATGACCCAGACT
                                                    ||  ||||||||||||||| ||
    CAGACTCAGGTCTTTGTATACATGTTGCTGTGGTTGTCTGGTGGTGATGGAGACATTGTGATGACCCAGTCT
      40        50        60        70        80      X 90      100

           30        40        50        60        70        80        90
    CCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
    |  |||||| ||      |||| |||||||||||| | | | |||||||||||||||||||| ||||  || |
    CAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCAGTCAGAATGTGGGTACT
  110       120       130       140       150       160       170       180

      100       110       120       130       140       150       160
    GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
```

```
 ||||||| ||||| |||||||| |||||||| |||||||||   ||||| || |  |||||| | || |||
AATGTAGCCTGGTATCAACAGAAACCAGGGCAATCTCCTAAAACACTGATTTACTCGGCATCCTACCGTTAC
      190       200       210       220       230       240       250

  170       180       190       200       210       220       230
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAG
| ||||||||||||||||||||| |||||||||| | |||| ||||||||| |||||||||||| |||||||
AGTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTAGGACAGATTTCACTCTCACCATCAGCAATGTGCAG
     260       270       280       290       300       310       320

240       250       260       270       280       290       300
GCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAG
 ||||||||  ||||||  ||||||||||||||  || | |||| ||| |  |||||||| || || ||||||
TCTGAAGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCTTGGACGTTCGGTGGAGGCACCAAG
   330       340       350       360       370       380       390

 310       X
  CTGGAGATC
  ||||| |||
  CTGGAAATCAAACGG
   400    X  410
```

11. US-07-977-702-2 (1-318)
    N40022 cDNA insert of pK17G4 encoding kappa anti-carcinoe

```
 ID   N40022 standard; cDNA; 882 BP.
 AC   N40022;
 DT   01-DEC-1991  (first entry)
 DE   cDNA insert of pK17G4 encoding kappa anti-carcinoembryonic antigen.
 KW   Immunoglobulin; ds DNA; carcinoembryonic antigen; vector pK17G4.
 PN   EP-125023-A.
 PD   14-NOV-1984.
 PF   06-APR-1984; 302368.
 PR   08-APR-1983; US-483457.
 PA   (CITY) City of Hope.
 PA   (GETH) Genentech Inc.
 PI   Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD.
 DR   WPI; 84-283749/46.
 PT   Immunoglobulin(s) produced by recombinant host cells - useful as
 PT   antibodies analogous to forms from mammals.
 PS   Disclosure; Fig. 2A-B; 79pp; English.
 CC   The cDNA is contained within recombinant vector pK17G4 and encodes
 CC   kappa anti-carcinoembryonic antigen chain. Using the vector the
 CC   immunoglobulin is produced readily in pure monoclonal form. Genetic
 CC   manipulations can be used to produce chimeras of variants drawing
 CC   their homology from species differing from each other. Protein
 CC   manipulation is also possible.
 SQ   Sequence   882 BP;   231 A;   243 C;   194 G;   214 T;

Initial Score    =   252  Optimized Score  =   254  Significance = 18.29
Residue Identity =   79%  Matches          =   255  Mismatches   =   63
Gaps             =     1  Conservative Substitutions             =     0

                          X        10        20        30        40
                          AG-TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGC
                          ||  ||||||||||||||| ||| ||||||| ||      ||||
GTTGCTGTGGTTGTCTGGTGTTGAAGGAGACATTGTGATGACCCAGTCTCACAAATTCATGTCCACATCAGT
        10        20        30        40        50        60        70

    50        60        70        80        90       100       110
AGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAA
||||||||||||  | ||| ||||||||||||||||||  ||||  |  || | |||| ||||| ||||||||
AGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGGGTGCTGCTATAGCCTGGTATCAACAGAA
      80        90       100       110       120       130       140
```

```
   120       130       140       150       160       170       180
   GCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCAC
    ||||| || |||||||||||| ||||| || | |||||||  ||  |||||||||||||||||||||||||
   ACCAGGACAATCTCCTAAACTACTGATTTACTGGGCATCCACCCGGCACACTGGAGTCCCTGATCGCTTCAC
      150       160       170       180       190       200       210

  190       200       210       220       230       240       250       260
   TGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTT
    |||||||||| |||||| ||||||||| ||||||| |||| ||||||| |||| ||| |||||| ||||||
   AGGCAGTGGATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGATGACTTGGCAGATTATTT
    220       230       240       250       260       270       280

          270       280       290       300       310       X
   CTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGATC
   |||||| ||  ||    | | |||   ||||||||| |  |||||||||||||| |
   CTGTCAACAATATAGCGGGTATCCTCTCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAACGGGCTGATGC
  290       300       310       320       330       340     X 350       360

   TGCACCAACTGTATCCATCTTCCCACCATCCAGTGA
          370       380       390
```

12. US-07-977-702-2 (1-318)
    Q04264 Encodes Colon Cancer monoclonal antibody CC83 ligh

```
 ID   Q04264 standard; DNA; 685 BP.
 AC   Q04264;
 DT   13-SEP-1990  (first entry)
 DE   Encodes Colon Cancer monoclonal antibody CC83 light chain variable region
 KW   chimeric antibodies; TAG72; light chain variable region;
 KW   heavy chain variable region; ss
 OS   synthetic.
 FH   Key             Location/Qualifiers
 FT   intron          136..313
 FT   /*tag= a
 FT   transit_peptide 76..325
 FT   /*tag=  b
 FT   /note="intron is spliced out"
 FT   misc_feature    326..610
 FT   /*tag=  c
 FT   /label= encodes variable segment
 FT   misc_feature    611..646
 FT   /*tag=  d
 FT   /label=encodes J4 segment
 PN   EP-365997-A.
 PD   02-MAY-1990.
 PF   18-OCT-1989; 119361.
 PR   19-OCT-1988;US-259943.
 PA   (DOWC) Dow Chemical Co.
 PI   Mezes P, Gourlie B, Rixon M;
 DR   WPI; 90-133521/18.
 DR   P-PSDB; R04387.
 PT   Chimeric antibodies against TAG72 and conjugate to provide imaging
 PT   markers and therapeutic tools
 PS   Disclosure; pp; English.
 CC   The polypeptide encoded by this sequence forms part of a chimera. The
 CC   other components are a heavy chain variable region and human-derived
 CC   constant light and heavy chain regions. The variable regions have
 CC   high affinity for TAG72. The constant regions reduce the side-effects
 CC   when administered to human patients because they are of human origin.
 CC   See also Q04258-63 and Q04265-9.
 SQ   Sequence   685 BP;   187 A;   138 C;   153 G;   207 T;

Initial Score    =    250  Optimized Score  =    253  Significance = 18.13
Residue Identity =    79%  Matches         =    254  Mismatches   =    64
Gaps             =      1  Conservative Substitutions             =      0
```

```
                                                    X         10        20
                                                    AG-TATTGTGATGACCCAGACT
                                                    ||  ||||||||||||||| ||
   TATGTGTGAGTTTATACACATTATCTGTTTCTGTTTGCAGGTGTTGAAGGAGACATTGTGATGACCCAGTCT
      280       290       300       310       320    X  330       340

          30        40        50        60        70        80        90
   CCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
   | ||||||| ||   |  ||||  |||||||||||| | ||| ||||||||||||||||||  |||| ||| |
   CACAAATTCATGTCCGCATCAGTGGGAGACAGGGTCAACATCACCTGCAAGGCCAGTCAGTATGTGGCTACT
    350       360       370       380       390       400       410

       100       110       120       130       140       150       160
   GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
   | ||||||| ||||  || || || ||||| |||||||||||||| ||||| ||    |||||||  ||  ||
   GCTGTAGCCTGGTTTCAGCATAAACCAGGTCAGTCTCCTAAACTACTGATTTACGGGGCATCCACCCGGCAC
  420       430       440       450       460       470       480       490

     170       180       190       200       210       220       230
   ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAG
   |||||||||||||||||||||||| |||||||||| |||||| ||||||||| ||| ||| |||| |||||||
   ACTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCATCATTAGCAATGTGCAG
          500       510       520       530       540       550       560

   240       250       260       270       280       290       300
   GCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAG
    |||| ||| |||||| |||||| ||||||||  ||    ||| ||| | |||||||||   |||||| |||
   TCTGAGGACTTGGCAGATTATTTGTGTCAGCATTATAGCGGCTATCCATTCACGTTCGGCTCGGGGACAAAG
        570       580       590       600       610       620       630

  310       X
    CTGGAGATC
     |||| ||
   TTGGAAATAAAACGTAAGTAGACTTTTGCTCATTTACTTGTGACGTTTTGG
      640  X    650       660       670       680
```

13. US-07-977-702-2 (1-318)
    N40023 mRNA encoding kappa anti-carcinoembryonic antigen.

```
 ID   N40023 standard; mRNA; 882 BP.
 AC   N40023;
 DT   01-DEC-1991  (first entry)
 DE   mRNA encoding kappa anti-carcinoembryonic antigen.
 KW   Immunoglobulin; ss mRNA; carcinoembryonic antigen.
 FH   Key             Location/Qualifiers
 FT   CDS             1..673
 FT   /*tag=  a
 PN   EP-125023-A.
 PD   14-NOV-1984.
 PF   06-APR-1984; 302368.
 PR   08-APR-1983; US-483457.
 PA   (CITY) City of Hope.
 PA   (GETH) Genentech Inc.
 PI   Cabilly S, Holmes WE, Wetzel RB, Heyneker HL, Riggs AD.
 DR   WPI; 84-283749/46.
 DR   P-PSDB; P40031.
 PT   Immunoglobulin(s) produced by recombinant host cells - useful as
 PT   antibodies analogous to forms from mammals.
 PS   Disclosure; Fig. 3; 79pp; English.
 CC   The mRNA is the coding sequence of the cDNA fragment contained within
 CC   recombinant vector pK17G4 (see N40022). It encodes kappa anti-
 CC   carcinoembryonic antigen chain. Using the vector the immunoglobulin is
 CC   produced readily in pure monoclonal form. Genetic manipulations can be
 CC   used to produce chimeras of variants drawing their homology from species
```

```
CC   Differing from each other. Protein manipulation is also possible.
SQ   Sequence   882 BP;    231 A;    244 C;    194 G;    213 U;

Initial Score    =    249  Optimized Score  =    253  Significance = 18.06
Residue Identity =    59%  Matches          =    254  Mismatches   =    64
Gaps             =      1  Conservative Substitutions              =     0

                           X        10        20        30        40
                           AG-TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGC
                           ||  ||||||||||||||| ||| ||||||| ||      ||||
   GUUGCUGUGGUUGUCUGGUGUUGAAGGAGACAUUGUGAUGACCCAGUCUCACAAAUUCAUGUCCACAUCAGU
           10        20        30        40        50        60        70

       50        60        70        80        90       100       110
   AGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAA
   |||||||||||| | ||| ||||||||||||||||||  ||||  |  || | |||| ||||| ||||||||
   AGGAGACAGGGUCAGCAUCACCUGCAAGGCCAGUCAGGAUGUGGGUGCUGCUAUAGCCUGGUAUCAACAGAA
         80        90       100       110       120       130       140

    120       130       140       150       160       170       180
   GCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCAC
    ||||| || |||||||||||| ||||| || |  |||||||  ||  ||||||||||||||||||||||||
   ACCAGGACAAUCUCCUAAACUACUGAUUUACUGGGCAUCCACCCGGCACACUGGAGUCCCUGAUCGCUUCAC
      150       160       170       180       190       200       210

  190       200       210       220       230       240       250       260
   TGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTT
    ||||||||||  ||||||  |||||||||  |||||||  ||||  |||||||  ||||  |||  ||||||  ||||||
   AGGCAGUGGAUCUGGGACAGAUUUCACUCUCACCAUUAGCAAUGUGCAGUCUGAUGACUUGGCAGAUUAUUU
    220       230       240       250       260       270       280

          270       280       290       300       310       X
   CTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGATC
   ||||||  ||  ||    | |  |||   |||||||||  |  ||||||||||||  ||  |
   CUGUCAACAAUAUAGCGGGUAUCCUCUCACGUUCGGUGCUGGGACCAAGCUGCAGCUGAAACGGGCUGAUGC
  290       300       310       320       330       340     X 350       360

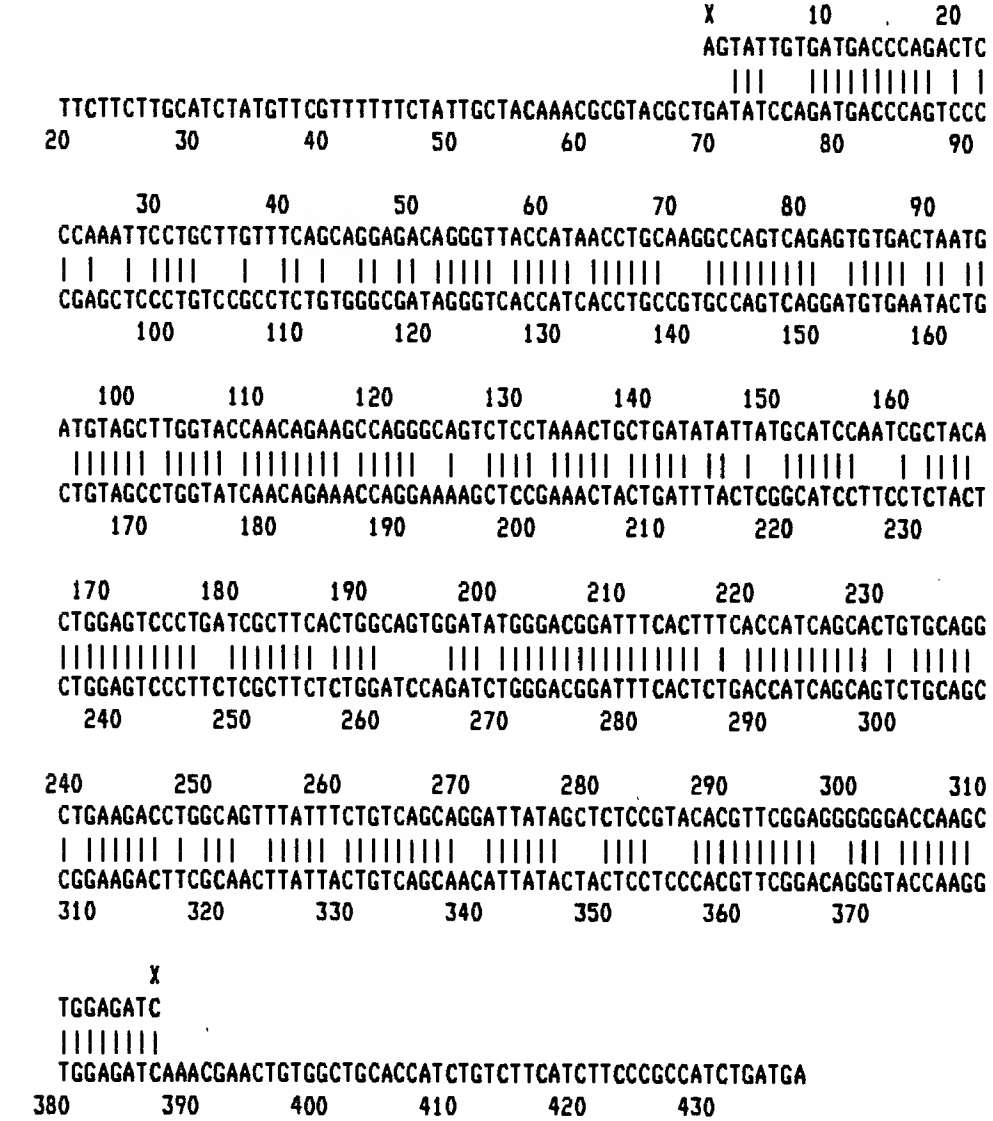
   UGCACCAACUGUAUCCAUCUUCCCACCAGCCAGUGA
          370       380       390


14. US-07-977-702-2 (1-318)
    Q25592       Encodes 4D5 Fab IgG antibody - recognises HER-2 re

 ID   Q25592 standard; DNA; 2178 BP.
 AC   Q25592;
 DT   08-DEC-1992  (first entry)
 DE   Encodes 4D5 Fab IgG antibody - recognises HER-2 receptor.
 KW   humanised IgG antibody; human growth hormone; hGH; selection;
 KW   screening; ss.
 OS   Homo sapiens.
 FH   Key             Location/Qualifiers
 FT   exon            1..712
 FT   /*tag=  a
 FT   /product= light chain
 FT   exon            796..2178
 FT   /*tag=  b
 FT   /product= heavy chain
 PN   WO9209690-A.
 PD   11-JUN-1992.
 PF   03-DEC-1991; U09133.
 PR   03-DEC-1990; US-621667.
 PR   10-APR-1991; US-683400.
 PR   14-JUN-1991; US-715300.
 PR   08-AUG-1991; US-743614.
 PA   (GETH ) GENENTECH INC.
```

PI Bass S, Garrard LJ, Greene R, Henner DJ, Lowman HB;
PI Matthews DJ, Wells JA;
DR WPI; 92-217069/26.
DR P-PSDB; R24047,8.
PT Selecting and enriching variant proteins - comprises fusing gene
PT encoding e.g. growth hormone to part of M13 phage coat protein
PT and mutagenising fusion prior to selection
PS Claim 46; Fig 11; 102pp; English.
CC This sequence encodes the Fab portion of the 4D5 humanised IgG
CC antibody that recognises the HER-2 receptor. It was inserted into
CC the plasmid pS0132, which had the DNA encoding human growth hormone
CC excised from it. The plasmid was used to transform E. coli SR101.
CC The sequence encodes two genes. The first encodes the variable and
CC constant regions of the light chain, and with the st II signal
CC sequence at its 5' end. The second contains four regions - the st II
CC signal sequence at its 5' end, the variable domain ofthe heavy chain,
CC the first domain of the heavy chain constant region, followed by the
CC M13 gene III.
SQ Sequence 2178 BP; 498 A; 572 C; 549 G; 559 T;

Initial Score = 234 Optimized Score = 237 Significance = 16.89
Residue Identity = 74% Matches = 237 Mismatches = 81
Gaps = 0 Conservative Substitutions = 0



15. US-07-977-702-2 (1-318)
Q28747 Anti-CEA specific light chain variable region DNA.

ID Q28747 standard; DNA; 387 BP.
AC Q28747;

DT 01-MAR-1993 (first entry)
DE Anti-CEA specific light chain variable region DNA.
KW Human; carcinoembryonic antigen; heavy chain; light chain; variable;
KW region; diagnostic; tumour; markers; targetting; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..387
FT /*tag= b
PN J04234987-A.
PD 24-AUG-1992.
PF 28-DEC-1990; 408810.
PR 28-DEC-1990; JP-408810.
PA (MITU) MITSUBISHI KASEI CORP.
DR WPI; 92-327631/40.
DR P-PSDB; R27054.
PT New DNA fragments encoding variable regions of ABS specific for
PT human CEA - for diagnosing and monitoring tumours, as tumour
PT markers and for treatment of tumours
PS Claim 1; Fig 2; 7pp; Japanese.
CC The anti-CEA murine monoclonal antibody light chain variable region
CC was obtd. by screening a cDNA library prepd. from mRNA obtd. from
CC hybridomas producing anti-CEA-specific antibodies with a probe
CC based on the constant region of the L-chain. The antibodies reacts
CC specifically with human CEA and are useful as a diagnostic agents,
CC as tumour markers for digestive organs, for diagnosis of malignant
CC tumours; for monitering after cancer operations, to follow up bloodless
CC therapy or as therapeutic agents in passive immune therapy and
CC targetting therapy. See also Q28744-6.
SQ Sequence 387 BP; 105 A; 92 C; 95 G; 95 T;

Initial Score = 227 Optimized Score = 257 Significance = 16.34
Residue Identity = 80% Matches = 260 Mismatches = 58
Gaps = 4 Conservative Substitutions = 0

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                                                ||  ||||||||||||||| ||
    CAGACTCAGGTCTTTCTATACATCTTGCTGTGGTTGTCTGGTGTTGATGGAGACATTGTGATGACCCAGTCT
  10        20        30        40        50        60        70        80

         30        40        50        60        70        80        90
    CCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
    |  ||||||  ||      ||||  |||||||||||||  | | | ||||||||||||||||||||  ||||  || |
    CAAAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCGTCACCTGCAAGGCCAGTCAGAATGTGGGTACT
         90       100       110       120       130       140       150

       100       110       120       130       140       150       160
    GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
     |||||||  |||||  ||||||||  ||||||||  |||||||||   |||||  | |  ||||||  | ||  |||
    AATGTAGCCTGGTATCAACAGAAACCAGGGCAATCTCCTAAAGCACTGATTAACTCGGCATCCTACCGGTAC
       160       170       180       190       200       210       220

     170       180       190       200       210       220       230
    ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAG
    | ||||||||||||||||||||  ||||||||||  ||||||  |||||||||  ||||||||||||  |||||  |
    AGTGGAGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCGG
      230       240       250       260       270       280       290

    240       250       260       270       280          290       300
    GCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCT---CTCCGTACACGTTCGGAGGGGGGACC
     ||||||||  |||||||  ||||||||||||||  || | ||||   |||  |||||  ||||||||||| |||
    TCTGAAGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATCCTCTCTACACATTCGGAGGGGGCACC
    300       310       320       330       340       350       360
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  310       X
   AAGCTGGAGATC
   || ||||| ||
   AACCTGGAAATAAAACGG
 370       380
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> 0 <
0| |0  IntelliGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-07-977-702-2.res made by shears on Tue 15 Jun 93 11:04:41-PDT.


Query sequence being compared:US-07-977-702-2 (1-318)
Number of sequences searched:               125798
Number of scores above cutoff:                4066

     Results of the initial comparison of US-07-977-702-2 (1-318) with:
   Data bank : EMBL-NEW 3, all entries
   Data bank : GenBank 75, all entries
   Data bank : GenBank-NEW 3, all entries
   Data bank : UEMBL 34_75, all entries
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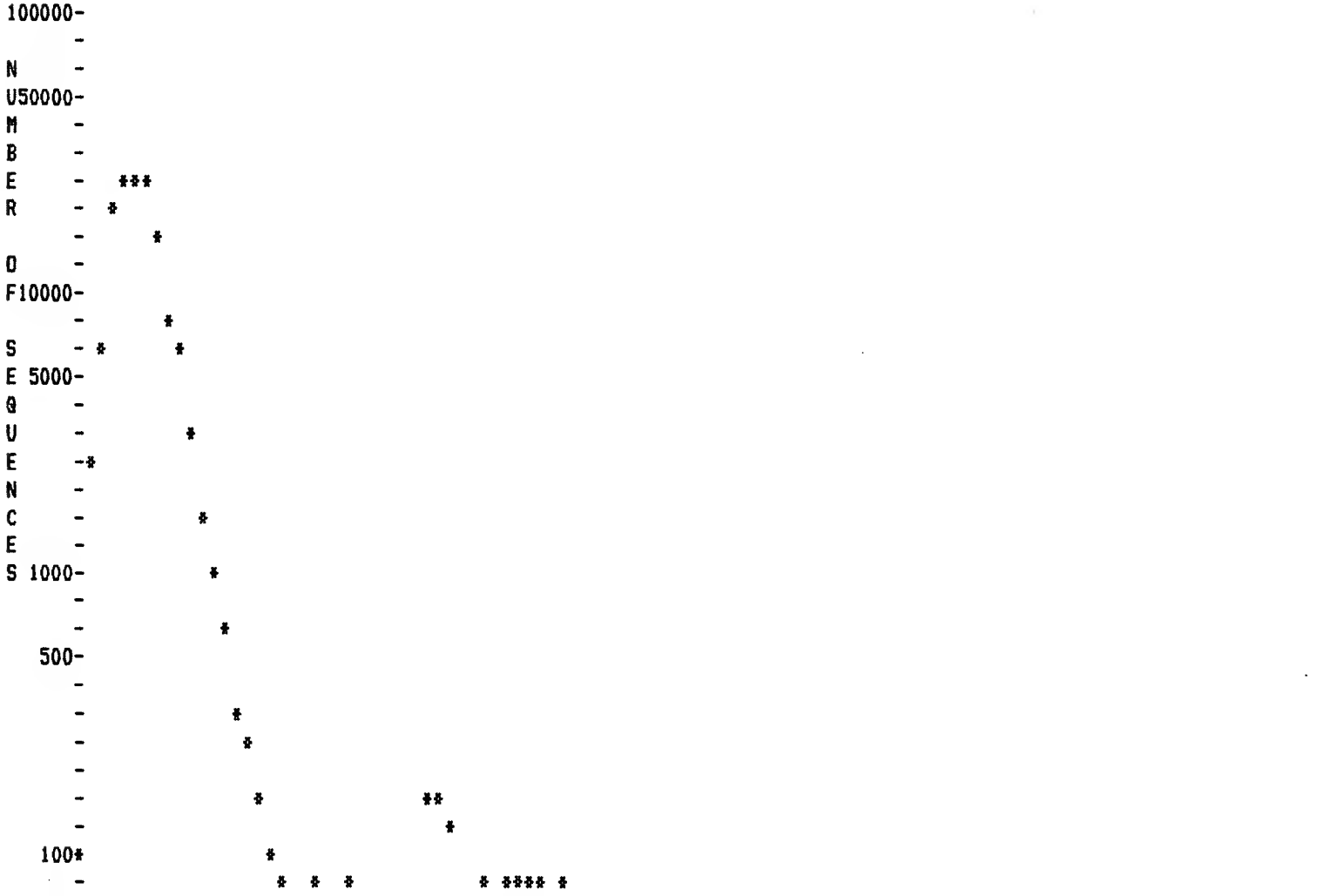

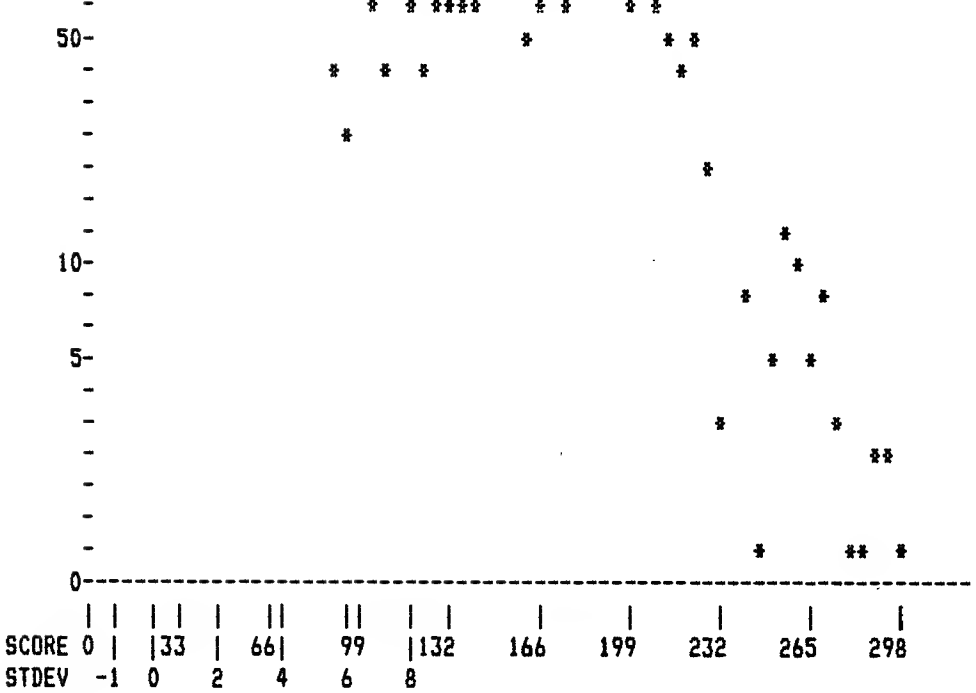

PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	1.00	Window size	32
Gap size penalty	0.33		
Cutoff score	0		
Randomization group	0		
Initial scores to save	40	Alignments to save	15
Optimized scores to save	0	Display context	50

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	27	27	11.35

Times:	CPU	Total Elapsed
	00:28:23.05	00:58:37.00

Number of residues: 150464018
Number of sequences searched: 125798
Number of scores above cutoff: 4066

Cut-off raised to 21.
Cut-off raised to 26.
Cut-off raised to 29.
Cut-off raised to 32.
Cut-off raised to 34.
Cut-off raised to 36.
Cut-off raised to 39.
Cut-off raised to 41.
Cut-off raised to 43.
Cut-off raised to 46.
Cut-off raised to 49.
Cut-off raised to 52.
Cut-off raised to 56.

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
	**** 23 standard deviations above mean ****					
1. MUSOHP57K	Mus musculus mRNA for Ig kapp	322	298	300	23.87	0
2. S63304	Vk28 VkJk [not specified, Gen	322	295	297	23.61	0
3. MUSSCETK	Mus musculus DNA for Ig kappa	322	295	297	23.61	0
4. MMIGRF28	Murine MRL-RF28L mRNA for IgM	398	295	298	23.61	0
5. MUSIGKCPF	Mouse Ig active kappa-chain (	938	290	293	23.17	0
6. MMIGKL	Mouse mRNA for Ig C.C58 M75 k	938	290	293	23.17	0
	**** 22 standard deviations above mean ****					
7. S60946	mAb BA.N4:4.57 V kappa region	300	287	289	22.91	0
8. MMVL105	Mouse mRNA for kappa-immunogl	321	287	290	22.91	0
9. MUSIGKVM	Mouse Ig germline kappa-chain	1816	280	294	22.29	0
10. S60873	Ab2 kappa chain V region [mA	300	278	279	22.11	0
	**** 21 standard deviations above mean ****					
11. MMNPCRLB6	M.musculus NPCRLB6 mRNA for i	321	273	275	21.67	0
12. MUSIGKCNK	Mouse Ig rearranged kappa-cha	456	272	275	21.58	0
13. MMNPCRLB1	M.musculus NPCRLB1 mRNA for i	321	271	273	21.50	0
14. MUSIGKVN	Mouse Ig germline kappa-chain	2002	270	284	21.41	0
15. MUSIGKCKP	Mouse Ig kappa-chain mRNA V-r	341	269	272	21.32	0
16. MUSIGLAFF	Mouse Ig kappa-chain mRNA V r	318	268	271	21.23	0
17. S51704	hybridoma antibody kappa-chai	313	266	266	21.06	0
18. MUSIGKAFQ	Mouse Ig active kappa-chain m	313	266	266	21.06	0
19. MUSIGLAFD	Mouse Ig kappa-chain mRNA V r	315	266	266	21.06	0
20. MUSIGKAL	Mouse Ig active kappa gene: M	739	266	269	21.06	0
	**** 20 standard deviations above mean ****					
21. MMVL3190	Mouse mRNA for kappa-immunogl	321	264	264	20.88	0
22. MUSIGKCSR	Mouse Ig active kappa-chain m	321	262	265	20.70	0
23. MUSIGKAAV	Mouse Ig rearranged kappa-cha	363	262	270	20.70	0
24. MUSIGKAQ	Mouse Ig kappa active gene: k	765	261	263	20.61	0
25. S51746	hybridoma antibody kappa-chai	276	260	261	20.53	0
26. MUSIGKAFV	Mouse Ig active kappa-chain m	275	259	260	20.44	0
27. MMBV1745L	M.musculus light chain variab	324	259	261	20.44	0
28. MUSIGKAJ	mouse ig kappa mrna from mopc	943	259	262	20.44	0
29. MMIGK9	Messenger RNA for mouse immun	943	259	262	20.44	0
30. MUSIGKAJA	Mouse Ig kappa active mRNA fr	462	258	261	20.35	0
31. MUSNC41	Mus musculus NC41 mRNA, parti	324	257	260	20.26	0
32. MMIGKV	Mouse mRNA for immunoglobulin	462	257	259	20.26	0
33. M245877S1	anti-human erbB-2 receptor bi	894	257	260	20.26	0
34. MUSIGKAED	Mouse Ig active kappa chain m	321	256	258	20.17	0
35. MUSIGLAA	Mouse rearranged light chain	354	256	260	20.17	0
36. HUMIGLIA	Human Ig light chain VJ regio	618	256	258	20.17	0
37. S115039	immunoglobulin light chain va	411	255	259	20.09	0
	**** 19 standard deviations above mean ****					
38. MUSIGKCNM	Mouse Ig active kappa chain m	321	254	259	20.00	0
39. MUSIGLAB	Mouse rearranged light chain	357	254	260	20.00	0
40. MUSIGLAFE	Mouse Ig kappa-chain mRNA V r	303	253	257	19.91	0

1. US-07-977-702-2 (1-318)
   MUSOHP57K Mus musculus mRNA for Ig kappa chain precursor.

LOCUS MUSOHP57K 322 bp ss-mRNA ROD 11-NOV-1992
DEFINITION Mus musculus mRNA for Ig kappa chain precursor.
ACCESSION D12733
KEYWORDS Ig kappa chain; steroid specific antibody; variable region.
SOURCE Mus musculus (strain BALB/c) hybridoma cell line OHP57.G6.1 mRNA.
  ORGANISM Mus musculus
  Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae.
REFERENCE 1 (bases 1 to 322)
  AUTHORS Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.

```
  TITLE     Molecular characterization of monoclonal anti-steroid antibodies:
            primary structures of the variable regions of seven antibodies
            specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and
            their pH-reactivity profiles
  JOURNAL   Mol. Immunol. 28, 1063-1072 (1991)
  STANDARD  full automatic
COMMENT     Submitted (27-JUL-1992) to DDBJ by: Jun-ichi Sawada
            Dept. of Biochem. and Immunochem.
            National Institute of Hygienic Sciences
            1-18-1 Kamiyoga
            Setagaya, Tokyo 158
            Japan
            Phone:  03-3700-1141 x240
            Fax:    03-3707-6950.
FEATURES             Location/Qualifiers
     mat_peptide     1..>322
                     /product="Ig kappa chain"
                     /codon_start=1
                     /note="VJ region (1-322)"
     CDS             <1..>322
                     /product="Ig kappa chain precursor"
                     /codon_start=1
                     /translation="SIVMTQTPKFLLIRAGDRVTMTCKASQSARNGVAWYQQKPGQSP
                     KLLIYYTSDRYTGVPDRFTGSGYGTDFTFTISTVQAEDVAVYFCQQVYSSPYTFGGGT
                     KLEIK"
BASE COUNT       86 a     76 c     84 g     76 t
ORIGIN

Initial Score    =    298  Optimized Score  =    300  Significance = 23.87
Residue Identity =    94%  Matches          =    300  Mismatches   =    18
Gaps             =      0  Conservative Substitutions               =     0

    X       10        20        30        40        50        60        70
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
    |||||||||||||||||||||||||||||||||| |   ||||||||||||||| ||||| |||||||||
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTATAAGAGCAGGAGACAGGGTCACCATGACCTGCAAG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
    |||||||||||||  ||  |||| ||||||||||||||||||||||||||||||||||||||||||||||||
    GCCAGTCAGAGTGCGAGAAATGGTGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
    ||  |||  |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TACTATACATCCGATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
    |||||||||||||||||||||||||||||| ||||||||||||||||||||||| |||||| |||||||||
    TTCACCATCAGCACTGTGCAGGCTGAAGACGTGGCAGTTTATTTCTGTCAGCAGGTTTATAGTTCTCCGTAC
     220       230       240       250       260       270       280

   290       300       310       X
    ACGTTCGGAGGGGGGACCAAGCTGGAGATC
    |||||||||||||||||||||||||| ||
    ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAAC
   290       300       310       320


2. US-07-977-702-2 (1-318)
   S63304       Vk28 VkJk [not specified, Genomic, 322 nt]
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```
LOCUS       S63304        322 bp    DNA             DNA       03-JAN-1992
DEFINITION  Vk28 VkJk [not specified, Genomic, 322 nt]
ACCESSION   S63304
KEYWORDS    .
SOURCE      not specified
  ORGANISM  Unclassified.
            Unclassified.
REFERENCE   1  (bases 1 to 322)
  AUTHORS   Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.
  TITLE     Molecular characterization of monoclonal anti-steroid antibodies:
            primary structures of the variable regions of seven antibodies
            specific for 17 alpha-hydroxyprogesterone or 11-deoxycortisol and
            their pH-reactivity profiles.
  JOURNAL   Mol. Immunol. 28, 1063-1072 (1991)
  STANDARD  full automatic
COMMENT     This entry [NCBI gibbsq 63304] was created by the journal scanning
            component of NCBI/GenBank at the National Library of Medicine.
            This sequence comes from Fig 5.
FEATURES             Location/Qualifiers
     CDS             1..322
                     /partial
                     /note="Description: Vk28 VkJk;  kappa chain variable and
                     joining region;  For the protein sequence (NCBI gibbsq
                     63309);  Method: conceptual translation with partial
                     peptide sequencing.  This sequence comes from Fig 6."
                     /product="monoclonal antibody SCET.M8.1"
                     /codon_start=1
                     /translation="SIVMT@TPKFLHVSVGDRVTITCKAS@SVRNAVVWY@@KTGLSP
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                     KLEIK"
BASE COUNT       87 a     72 c     84 g     79 t
ORIGIN
```

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Initial Score    =    295  Optimized Score  =    297  Significance = 23.61
Residue Identity =    93%  Matches          =    297  Mismatches   =    21
Gaps             =      0  Conservative Substitutions               =     0

   X       10        20        30        40        50        60        70
   AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
   |||||||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||||||||||||||
   AGTATTGTGATGACCCAGACTCCCAAATTCCTGCATGTATCAGTAGGAGACAGGGTTACCATAACCTGCAAG
   X       10        20        30        40        50        60        70

         80        90       100       110       120       130       140
   GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
   ||||||||||||||||  |||| ||||| |||||||||||||||| |||||| |||||||| ||||||||||
   GCCAGTCAGAGTGTGAGGAATGCTGTAGTTTGGTACCAACAGAAGACAGGGCTGTCTCCTAGACTGCTGATA
         80        90       100       110       120       130       140

      150       160       170       180       190       200       210
   TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
   || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   TACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
      150       160       170       180       190       200       210

    220       230       240       250       260       270       280
   TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
    |||||||||| | |||| ||||||||||||||||||||||||||||||||||| ||| ||  |||||||||
   CTCACCATCAGAAGTGTGGAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGAATTTTAAGTCTCCGTAC
    220       230       240       250       260       270       280

  290       300       310       X
   ACGTTCGGAGGGGGGACCAAGCTGGAGATC
   |||||||||||||||||||||||||| ||
   ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAAC
  290       300       310       320
```

3. US-07-977-702-2 (1-318)
MUSSCETK Mus musculus DNA for Ig kappa chain precursor.

```
LOCUS       MUSSCETK      322 bp ds-DNA             ROD       11-NOV-1992
DEFINITION  Mus musculus DNA for Ig kappa chain precursor.
ACCESSION   D12737
KEYWORDS    Ig kappa chain; steroid specific antibody; variable region.
SOURCE      Mus musculus (strain BALB/c) hybridoma cell line SCET.M8.1.1 DNA.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Mammalia; Rodentia; Muridae.
REFERENCE   1  (bases 1 to 322)
  AUTHORS   Sawada,J., Mizusawa,S., Terao,T., Naito,M. and Kurosawa,Y.
  TITLE     Molecular characterization of monoclonal anti-steroid antibodies:
            primary structures of the variable regions of seven antibodies
            specific for 17alpha-hydroxyprogesterone or 11-deoxycortisol and
            their pH-reactivity profiles
  JOURNAL   Mol. Immunol. 28, 1063-1072 (1991)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     mat_peptide     1..>322
                     /product="Ig kappa chain"
                     /codon_start=1
                     /note="VJ region (1-322)"
     CDS             <1..>322
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                     /codon_start=1
                     /translation="SIVMTQTPKFLHVSVGDRVTITCKASQSVRNAVVWYQQKTGLSP
                     RLLIYYASNRYTGVPDRFTGSGYGTDFTLTIRSVEAEDLAVYFCQQNFKSPYTFGGGT
                     KLEIK"
BASE COUNT       87 a     72 c     84 g     79 t
ORIGIN
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Initial Score    =    295  Optimized Score  =    297  Significance = 23.61
Residue Identity =    93%  Matches          =    297  Mismatches   =    21
Gaps             =      0  Conservative Substitutions              =     0

    X       10        20        30        40        50        60        70
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
    |||||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||||||||||||||
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCATGTATCAGTAGGAGACAGGGTTACCATAACCTGCAAG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
    ||||||||||||||||  |||| ||||| |||||||||||||||| |||||| |||||||| ||||||||||
    GCCAGTCAGAGTGTGAGGAATGCTGTAGTTTGGTACCAACAGAAGACAGGGCTGTCTCCTAGACTGCTGATA
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
    || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    TACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
     |||||||||| | |||| ||||||||||||||||||||||||||||||||||| ||| ||  |||||||||
    CTCACCATCAGAAGTGTGGAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGAATTTTAAGTCTCCGTAC
     220       230       240       250       260       270       280

   290       300       310       X
    ACGTTCGGAGGGGGGACCAAGCTGGAGATC
    |||||||||||||||||||||||||||| ||
    ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAAC
```

290 300 310 320

4. US-07-977-702-2 (1-318)
MMIGRF28 Murine MRL-RF28L mRNA for IgM (kappa)-light chain

```
LOCUS       MMIGRF28      398 bp    RNA            ROD       04-AUG-1992
DEFINITION  Murine MRL-RF28L mRNA for IgM (kappa)-light chain V(kappa)28,
            J(kappa) 1
ACCESSION   X14622
KEYWORDS    autoantibody; Ig kappa light chain; Ig light chain; IgM;
            immunoglobulin; variable region.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 398)
  AUTHORS   Kofler,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-1989) Kofler R., General and Experimental
            Pathology, University of Innsbruck, Fritz-Pregl-Str.3, A-6020
            Innsbruck, Austria.
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 362)
  AUTHORS   Kofler,R., Duchosal,M.A. and Dixon,F.J.
  TITLE     Complexity, polymorphism, and connectivity of mouse V-kappa gene
            families
  JOURNAL   Immunogenetics 29, 65-74 (1989)
  STANDARD  full automatic
COMMENT     *source: strain=MRL/Mp-lpr/lpr;
            *source: haplotype=Ig(kappa)(a);
            *source: tissue=spleen;
            *source: cell_type=hybridoma;
            *source: cell_line=MRL-RF28;

            Data kindly reviewed (24-jul-1989) by Kofler R.
FEATURES             Location/Qualifiers
     CDS             18..>398
                     /note="IgM;  (kappa)-light chain precursor"
                     /codon_start=1
                     /translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVTMTCK
                     ASQSVGNNVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED
                     LAVYFCQQHYSSPWTFGGGTKLEIK"
     CDS             18..77
                     /note="signal peptide;  (AA -20 to -1)"
                     /codon_start=1
                     /translation="MKSQTQVFIFLLLCVSGAHG"
     CDS             78..>398
                     /note="mature IgM;  (kappa)-light chain (AA 1-107)"
                     /codon_start=1
                     /translation="SIVMTQTPKFLPVSAGDRVTMTCKASQSVGNNVAWYQQKPGQSP
                     KLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYSSPWTFGGGT
                     KLEIK"
BASE COUNT      102 a     97 c    100 g     99 t
ORIGIN
```

```
Initial Score    =    295  Optimized Score  =    298  Significance = 23.61
Residue Identity =    93%  Matches          =    298  Mismatches   =    20
Gaps             =      0  Conservative Substitutions               =     0

                                                  X       10        20
                                                  AGTATTGTGATGACCCAGACTC
                                                  ||||||||||||||||||||||
   AGACCCAGGTCTTCATATTTCTACTGCTCTGTGTGTCTGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
    30        40        50        60        70        80        90
```

```
      30        40        50        60        70        80        90
   CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
   ||||||||||||| ||| |||||||||||||||||||||| |||||||||||||||||||||||  ||||
   CCAAATTCCTGCCTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGGTAATA
 100       110       120       130       140       150       160       170

     100       110       120       130       140       150       160
   ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
   ||||||| |||||||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
   ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACA
         180       190       200       210       220       230       240

    170       180       190       200       210       220       230
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
   |||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||| ||||||||
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTCACCATCAGCAGTGTGCAGG
      250       260       270       280       290       300       310

 240       250       260       270       280       290       300       310
   CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
    |||||||||||||||||||||||||||||| ||||||||||||||  |||||||| || || |||||||
   TTGAAGACCTGGCAGTTTATTTCTGTCAGCAGCATTATAGCTCTCCGTGGACGTTCGGTGGAGGCACCAAGC
     320       330       340       350       360       370       380

         X
   TGGAGATC
   |||| |||
   TGGAAATCAAA
   390    X
```

5. US-07-977-702-2 (1-318)
   MUSIGKCPF Mouse Ig active kappa-chain (V-J-C) mRNA from C.C5

```
LOCUS       MUSIGKCPF     938 bp ss-mRNA            ROD       15-SEP-1989
DEFINITION  Mouse Ig active kappa-chain (V-J-C) mRNA from C.C58 m75 myeloma.
ACCESSION   M12177
KEYWORDS    constant region; immunoglobulin light chain; immunoglobulin-kappa;
            joining region; processed gene; variable region.
SOURCE      Mouse C.C58 m75 myeloma cDNA to mRNA, clone p9.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 938)
  AUTHORS   Goldrick,M.M., Boyd,R.T., Ponath,P.D., Lou,S.Y. and Gottlieb,P.D.
  TITLE     Molecular genetic analysis of the VkSer group associated with two
            mouse light chain genetic markers
  JOURNAL   J. Exp. Med. 162, 713-728 (1985)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     sig_peptide     36..95
                     /codon_start=1
                     /note="Ig kappa chain (V-J-C) signal peptide"
     mat_peptide     96..737
                     /codon_start=1
                     /note="Ig kappa chain (V-J-C) mature peptide"
     misc_recomb     380..381
                     /note="V region end/J region start"
     misc_recomb     416..417
                     /note="J region end/C region start"
     CDS             36..739
                     /partial
                     /note="Ig kappa chain;  (V-J-C)"
                     /codon_start=1
                     /translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVTMTCK
                     ASQSVGNNVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED
```

```
                    LAVYFCQGAYTSPPTFGGGTKLEINRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFY
                    PKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATH
                    KTSTSPIVKSFNRNECX*
 BASE COUNT      248 a    260 c    206 g    224 t
 ORIGIN

Initial Score    =    290  Optimized Score  =    293  Significance = 23.17
Residue Identity =    92%  Matches          =    293  Mismatches   =    25
Gaps             =      0  Conservative Substitutions               =     0

                                                      X       10        20
                                                      AGTATTGTGATGACCCAGACTC
                                                      ||||||||||||||||||||||
    AGACCCAGGTCTTCATATTTCTACTGCTCTGTGTGTCTGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
       50        60        70        80        90     X 100       110

          30        40        50        60        70        80        90
    CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
    |||||||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||||  ||||
    CCAAATTCCTGCCTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGGTAATA
    120       130       140       150       160       170       180

       100       110       120       130       140       150       160
    ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
    ||||||| |||||||||||||||||||| |||||||||||| |||||||||| ||||||||||||||||||
    ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAATTGCTGATATACTATGCATCCAATCGCTACA
  190       200       210       220       230       240       250       260

     170       180       190       200       210       220       230
    CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
    |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||| ||||||||
    CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTCACCATCAGCAGTGTGCAGG
          270       280       290       300       310       320       330

   240       250       260       270       280       290       300       310
    CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
     |||||||||||||||||||||||||||||  |||||| ||||||    |||||||| || || |||||||
    TTGAAGACCTGGCAGTTTATTTCTGTCAGCAACATTATACCTCTCCTCCGACGTTCGGTGGAGGCACCAAGC
       340       350       360       370       380       390       400

            X
    TGGAGATC
    |||| |||
    TGGAAATCAATCGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGA
      410  X    420       430       440       450       460
```

6. US-07-977-702-2 (1-318)
   MMIGKL Mouse mRNA for Ig C.C58 M75 kappa light chain (VK

```
 LOCUS       MMIGKL        938 bp    RNA             ROD       07-MAY-1992
 DEFINITION  Mouse mRNA for Ig C.C58 M75 kappa light chain (VK Ser-group)
 ACCESSION   X02816 M12177
 KEYWORDS    constant region; Ig light chain; immunoglobulin; joining region;
             signal peptide; variable region.
 SOURCE      mouse
   ORGANISM  Mus musculus
             Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
             Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 REFERENCE   1  (bases 1 to 938)
   AUTHORS   Goldrick,M.M., Boyd,R.T., Ponath,P.D., Lou,S.Y. and Gottlieb,P.D.
   TITLE     Molecular genetic analysis of the VkSer group associated with two
             mouse light chain genetic markers
   JOURNAL   J. Exp. Med. 162, 713-728 (1985)
   STANDARD  full automatic
 COMMENT     BALB/C mice germline V(K1) region see MMIG25, C(K) region see
```

MMIGAC

Data kindly reviewed (24-FEB-1986) by P.D. Gottlieb.

```
FEATURES             Location/Qualifiers
     misc_feature    165..197
                     /note="put. CDR1"
     misc_feature    243..263
                     /note="put. CDR2"
     misc_feature    360..380
                     /note="put. CDR3"
     misc_feature    381..382
                     /note="CC is TG in germline J(K1) of BALB/ C"
     misc_feature    416
                     /note="T is A in germline J(K1) of BALB/C"
     misc_feature    710
                     /note="C is T in germline C(K) of BALB/C"
     CDS             36..737
                     /note="(K)L-chain precursor"
                     /codon_start=1
                     /translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVTMTCK
                     ASQSVGNNVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED
                     LAVYFCQQHYTSPPTFGGGTKLEINRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFY
                     PKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATH
                     KTSTSPIVKSFNRNEC"
     CDS             36..95
                     /note="signal peptide;  (aa -20 to -1)"
                     /codon_start=1
                     /translation="MKSQTQVFIFLLLCVSGAHG"
     CDS             96..737
                     /note="mature;  (K)L-chain (aa 1-214)"
                     /codon_start=1
                     /translation="SIVMTQTPKFLPVSAGDRVTMTCKASQSVGNNVAWYQQKPGQSP
                     KLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYTSPPTFGGGT
                     KLEINRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL
                     NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC"
     CDS             96..380
                     /note="V region"
                     /codon_start=1
                     /translation="SIVMTQTPKFLPVSAGDRVTMTCKASQSVGNNVAWYQQKPGQSP
                     KLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVEDLAVYFCQQHYTSP"
     CDS             381..416
                     /note="J region"
                     /codon_start=1
                     /translation="PTFGGGTKLEIN"
     CDS             417..737
                     /note="C region"
                     /codon_start=1
                     /translation="RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKID
                     GSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSF
                     NRNEC"
BASE COUNT      248 a    260 c    206 g    224 t
ORIGIN
```

```
Initial Score    =    290  Optimized Score  =    293  Significance = 23.17
Residue Identity =    92%  Matches          =    293  Mismatches   =    25
Gaps             =      0  Conservative Substitutions               =     0

                                                  X       10        20
                                                  AGTATTGTGATGACCCAGACTC
                                                  ||||||||||||||||||||||
   AGACCCAGGTCTTCATATTTCTACTGCTCTGTGTGTCTGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
     50        60        70        80        90     X 100       110

        30        40        50        60        70        80        90
   CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
   |||||||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||  ||||
```

```
   CCAAATTCCTGCCTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGGTAATA
   120       130       140       150       160       170       180

      100       110       120       130       140       150       160
   ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
   ||||||| |||||||||||||||||||| |||||||||||| |||||||||| ||||||||||||||||||
   ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAATTGCTGATATACTATGCATCCAATCGCTACA
 190       200       210       220       230       240       250       260

    170       180       190       200       210       220       230
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
   |||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||| ||||||||
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTCACCATCAGCAGTGTGCAGG
         270       280       290       300       310       320       330

  240       250       260       270       280       290       300       310
   CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGC
    |||||||||||||||||||||||||||||| |||||| ||||||    |||||||| || || |||||||
   TTGAAGACCTGGCAGTTTATTTCTGTCAGCAACATTATACCTCTCCTCCGACGTTCGGTGGAGGCACCAAGC
      340       350       360       370       380       390       400

          X
   TGGAGATC
   |||| |||
   TGGAAATCAATCGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGA
     410  X    420       430       440       450       460
```

7. US-07-977-702-2 (1-318)
   S60946 mAb BA.N4:4.57 V kappa region [mice, B cell hybrid

```
LOCUS       S60946        300 bp    mRNA            ROD       08-JAN-1992
DEFINITION  mAb BA.N4:4.57 V kappa region [mice, B cell hybridoma, BALB/c,
            mRNA, 300 nt]
ACCESSION   S60946
KEYWORDS    .
SOURCE      mice BALB/c B cell hybridoma
  ORGANISM  Unclassified.
            Unclassified.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Carlsson,L., Andersson,A. and Holmberg,D.
  TITLE     Germ-line origin of functional idiotypic interactions:
            identification of two idiotypically connected, natural antibodies
            that are encoded by germ-line gene elements.
  JOURNAL   Eur. J. Immunol. 21, 2285-2288 (1991)
  STANDARD  full automatic
COMMENT     This entry [NCBI gibbsq 60946] was created by the journal scanning
            component of NCBI/GenBank at the National Library of Medicine.
            This sequence comes from Fig.2.
FEATURES             Location/Qualifiers
     misc_feature    1..300
                     /note="This feature applies to a gene which lacks a coding
                     region feature. Description: mAb BA.N4:4.57 V kappa
                     region"
BASE COUNT       74 a     69 c     77 g     77 t      3 others
ORIGIN
```

```
Initial Score    =    287  Optimized Score  =    289  Significance = 22.91
Residue Identity =    96%  Matches          =    289  Mismatches   =    11
Gaps             =      0  Conservative Substitutions               =     0
```

```
   X       10        20        30        40        50        60        70
   AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
   |||||||||||||||||||||||| |||||||||||| |||||||||| ||||||||||||||||||||
   AGTATTGTGATGACCCAGACTCCNNAATTCCTGCTTGTATCAGCAGGAGAGAGGGTTACCATAACCTGCAAG
   X       10        20        30        40        50        60        70
```

```
       80        90       100       110       120       130       140
GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
|||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCAGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
       80        90       100       110       120       130       140

     150       160       170       180       190       200       210
TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
     150       160       170       180       190       200       210

     220       230       240       250       260       270       280
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
|||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGNAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTGG
     220       230       240       250       260       270       280

   290         X       310
    ACGTTCGGAGGGGGGACCAAGCTGGAGATC
    |||||||| ||
    ACGTTCGGTGGA
   290       300
```

8. US-07-977-702-2 (1-318)
   MMVL105 Mouse mRNA for kappa-immunoglobulin light chain V-

```
LOCUS       MMVL105       321 bp    RNA             ROD       04-AUG-1992
DEFINITION  Mouse mRNA for kappa-immunoglobulin light chain V-J region (cell
            line 105-2H)
ACCESSION   X51852
KEYWORDS    Ig kappa light chain; Ig light chain; immunoglobulin;
            joining region; variable region.
SOURCE      mouse
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
            Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Reininger,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-1990) Reininger L., Dept of Pathology , Centre
            Medical Universitaire, 1 rue michel servet, CH-1211 Geneve 4,
            Switzerland.
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 321)
  AUTHORS   Reininger,L., Shibata,T., Ozaki,S., Shirai,T., Jaton,J.C. and
            Izui,S.
  TITLE     Variable region sequences of pathogenic anti-mouse red blood cell
            autoantibodies from autoimmune NZB mice.
  JOURNAL   Eur. J. Immunol. 20, 771-777 (1990)
  STANDARD  full automatic
COMMENT     *source: strain=New Zealand black; *source: cell_type=hybridoma B;

            *source: cell_line=105-2H.
FEATURES             Location/Qualifiers
     CDS             <1..>321
                     /note="kappa-Ig light chain (107 AA)"
BASE COUNT       81 a     72 c     82 g     78 t      8 others
ORIGIN
```

```
Initial Score    =    287  Optimized Score  =    290  Significance = 22.91
Residue Identity =    91%  Matches          =    291  Mismatches   =    26
Gaps             =      1  Conservative Substitutions              =     0
```

```
 X       10        20        30        40        50        60        70
 AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAA
 || |||||| |||||||||||||  |||||||||||||| |||| |||||||||||||||||||||||||| |
GAG-ATTGTGTTGACCCAGACTCCNNAATTCCTGCTTGTATCAGTAGGAGACAGGGTTACCATAACCTGCNA
 X       10        20        30        40        50        60        70

       80        90       100       110       120       130       140
GGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGAT
|||||||||||||||||  ||||||||  |  |||||||||||| |||||||||||||||||||| |||||||
GGCCAGTCAGAGTGTGAAGAATGATGTTGGNTGGTACCAACAGNAGCCAGGGCAGTCTCCTAAATTGCTGAT
       80        90       100       110       120       130       140

    150       160       170       180       190       200       210
ATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCAC
||| |||||||||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||||
ATACTATGCATCCAATCGCTACACTGGAATCCCTGATCGCTTCACTGGCAGTGGACATGGGACGGATTTCAC
    150       160       170       180       190       200       210

  220       230       240       250       260       270       280
TTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTA
|||||||||||||||||||||||||||||||||  |||||||||||||||||||| ||| ||||||||
TTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGNNGTTTATTTCTGTCAGCAGGATNATACCTCTCCGTG
  220       230       240       250       260       270       280

290       300       310       X
CACGTTCGGAGGGGGGACCAAGCTGGAGATC
 |||||||| || ||||||||||||||| ||
GACGTTCGGTGGAGGGACCAAGCTGGAAATAAAA
290       300       310       320
```

9. US-07-977-702-2 (1-318)
   MUSIGKVM Mouse Ig germline kappa-chain V-region gene V-Ser.

```
LOCUS       MUSIGKVM     1816 bp ds-DNA             ROD       30-JUN-1987
DEFINITION  Mouse Ig germline kappa-chain V-region gene V-Ser.
ACCESSION   M14360
KEYWORDS    constant region; germline; immunoglobulin-kappa; variable region.
SOURCE      Mouse (Balb/c) liver DNA, clone EM3.BALB-1.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 1816)
  AUTHORS   Boyd,R.T., Goldrick,M.M. and Gottlieb,P.D.
  TITLE     Structural differences in a single gene encoding the V-k-Ser group
            of light chains explain the existence of two mouse light-chain
            genetic markers
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138 (1986)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     exon            <916..964
                     /number=1
                     /note="Ig kappa-chain precursor V-Ser"
     sig_peptide     join(916..964,1179..1189)
                     /codon_start=1
                     /note="Ig kappa-chain signal peptide"
     sig_peptide     916..964
                     /codon_start=1
                     /note="Ig kappa-chain signal peptide"
     intron          965..1178
                     /note="IgK intron A"
     exon            1179..>1474
                     /number=2
                     /note="Ig kappa-chain precursor V-Ser"
     sig_peptide     1179..1189
                     /codon_start=1
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```
                     /note="Ig kappa-chain signal peptide"
     mat_peptide     1190..1474
                     /partial
                     /codon_start=1
                     /note="Ig kappa-chain"
     iDNA            1475..>1816
                     /note="V-J intervening DNA (5' end +/- 1 bp)"
     CDS             join(916..964,1179..1473)
                     /partial
                     /partial
                     /note="Ig kappa-chain precursor V-Ser"
                     /codon_start=1
                     /translation="MKSQTQVFVFLLLCVSGAHGSIVMTQTPKFLLVSAGERVTITCK
                     ASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTDFTFTISTVQAED
                     LAVYFCQQDYSSP"
 BASE COUNT      482 a    385 c    354 g    595 t
 ORIGIN      1297 bp upstream of KpnI site; chromosome 6.

Initial Score    =    280  Optimized Score  =    294  Significance = 22.29
Residue Identity =    92%  Matches          =    301  Mismatches   =    17
Gaps             =      9  Conservative Substitutions               =     0

                                                  X       10        20
                                                  AGTATTGTGATGACCCAGACTC
                                                  ||||||||||||||||||||||
   GTGTAAATGTGTATCCTCATTATTTATCTCTGATTGCAGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
 1140      1150      1160      1170      1180      1190      1200      1210

         30        40        50        60        70        80        90
   CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
   |||||||||||||||| |||||||||| |||||||||||||||||||||||||||||||||||| |||||
   CCAAATTCCTGCTTGTATCAGCAGGAGAGAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATG
        1220      1230      1240      1250      1260      1270      1280

      100       110       120       130       140       150       160
   ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
   |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
   ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACA
      1290      1300      1310      1320      1330      1340      1350

    170       180       190       200       210       220       230
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
    1360      1370      1380      1390      1400      1410      1420

  240       250       260       270       280       290          300
   CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACAC-GTTC-GGAG-GGGGGAC-C
   |||||||||||||||||||||||||||||||||||||||||||||||||||   ||| || |   ||      || |
   CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCTCCCACAGTGCTTCAGCCTCCTACAC
  1430      1440      1450      1460      1470      1480      1490

       310       X
   AA----GCTGGAGA-TC
   ||     || |||| ||
   AAACCTCCTTGAGAGTCTCACAGCTGTGGCCTTGCACAGTTCCCCCTCTGCCTGGAGCAGCGATTCA
 1500      1510      1520      1530      1540      1550      1560


10. US-07-977-702-2 (1-318)
   S60873       Ab2 kappa chain V region | mAb F {V/J junction} [m

 LOCUS       S60873        300 bp    mRNA            ROD       08-JAN-1992
 DEFINITION  Ab2 kappa chain V region | mAb F {V/J junction} [mice, MLR-lpr/lpr,
             mRNA Partial, 300 nt]
 ACCESSION   S60873
```

KEYWORDS .
SOURCE mice MLR-lpr/lpr
ORGANISM Unclassified.
Unclassified.
REFERENCE 1 (bases 1 to 300)
AUTHORS Koizumi,T., Puccetti,A., Migliorini,P., Barrett,K.J. and Schwartz,R.S.
TITLE Molecular heterogeneity of auto-anti-idiotypic antibodies in MLR-lpr/lpr mice.
JOURNAL Eur. J. Immunol. 21, 2185-2193 (1991)
STANDARD full automatic
COMMENT This entry [NCBI gibbsq 60873] was created by the journal scanning component of NCBI/GenBank at the National Library of Medicine.
This sequence comes from Fig.6.
FEATURES Location/Qualifiers
misc_feature 1..300
/note="This feature applies to a gene which lacks a coding region feature. Description: Ab2 kappa chain V region | mAb F"
BASE COUNT 74 a 77 c 71 g 76 t 2 others
ORIGIN

Initial Score = 278 Optimized Score = 279 Significance = 22.11
Residue Identity = 93% Matches = 279 Mismatches = 21
Gaps = 0 Conservative Substitutions = 0

```
   X       10        20        30        40        50        60        70
   AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
   |||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||| |||||||||
   AGTATTGTGATGACCCAGACTCCCAAATTCCTGCCTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAG
   X       10        20        30        40        50        60        70

         80        90       100       110       120       130       140
   GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
   ||||||||||||||  |||| ||||||| |||||||||||||||||||| |||||||||| |||||||||
   GCCAGTCAGAGTGTGGGTAATAATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAANCTGCTGATA
         80        90       100       110       120       130       140

      150       160       170       180       190       200       210
   TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
   || |||||||||||||||||||||| |||||||||||||||||||||||||||||| |||||| |||||||||
   TACTATGCATCCAATCGCTACACTGGNGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACT
      150       160       170       180       190       200       210

    220       230       240       250       260       270       280
   TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
   |||||||||||||| |||||||| |||||||||||||||||||||||||||||||| |||||||||||| | |
   TTCACCATCAGCAGTGTGCAGGTTGAAGACCTGGCAGTTTATTTCTGTCAGCAGCATTATAGCTCTCCATTC
    220       230       240       250       260       270       280

  290         X       310
   ACGTTCGGAGGGGGGACCAAGCTGGAGATC
   ||||||||   |
   ACGTTCGGCACG
  290       300
```

11. US-07-977-702-2 (1-318)
MMNPCRLB6 M.musculus NPCRLB6 mRNA for immunoglobulin light c

ID MMNPCRLB6 standard; RNA; ROD; 321 BP.
XX
AC X70097; X51612;
XX
DT 19-MAR-1993 (Rel. 35, Created)
DT 19-MAR-1993 (Rel. 35, Last updated, Version 1)

```
XX
DE   M.musculus NPCRLB6 mRNA for immunoglobulin light chain, variable
DE   region
XX
KW   immunoglobulin light chain variable region.
XX
OS   Mus musculus (mouse)
OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC   Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
XX
RN   [1]
RP   1-321
RA   Izui S.;
RT   ;
RL   Submitted (05-FEB-1993) on tape to the EMBL Data Library by:
RL   S. Izui, Dept. of Pathology, Centre Medical Universitaire, 1, Rue
RL   Michel Servet, CH-1211, geneva 4, SWITZERLAND
XX
CC   *source: strain=C57BL/6;
CC   *source: tissue=lymphoid;
CC   *source: cell_type=hybridoma;
CC   *source: cell_line=CB6;
CC   *source: is_germline=N;
XX
FH   Key             Location/Qualifiers
FH
FT   CDS             <1..>321
FT                   /codon_start=1
FT                   /product="immunoglobulin light chain, variable region"
XX
SQ   Sequence 321 BP; 88 A; 80 C; 78 G; 75 T; 0 other;

Initial Score    =    273  Optimized Score  =    275  Significance = 21.67
Residue Identity =    86%  Matches          =    275  Mismatches   =    43
Gaps             =      0  Conservative Substitutions              =     0

    X       10        20        30        40        50        60        70
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
       ||||||||||||||| ||| ||||||| ||      |||| ||||||||||||| | ||| |||||||||
    GACATTGTGATGACCCAGTCTCACAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAG
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
    |||||||||  ||||| || || ||||||| ||||| |||||||| ||||| || ||||||||||| |||||
    GCCAGTCAGGATGTGAGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTACTGATT
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
    || |  |||||| | || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
    TACTCGGCATCCTACCGGTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACGGATTTCACT
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
    |||||||||||| |||||||||||||||||||||||||||| |||||||||  |||||||  ||||||||
    TTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCGTAC
     220       230       240       250       260       270       280

   290       300       310       X
    ACGTTCGGAGGGGGGACCAAGCTGGAGATC
    |||||||||||||||||||||||||| ||
    ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
   290       300       310       320
```

12. US-07-977-702-2 (1-318)
    MUSIGKCNK   Mouse Ig rearranged kappa-chain mRNA, clone AN12K.

```
LOCUS       MUSIGKCNK     456 bp ss-mRNA            ROD       15-MAR-1990
DEFINITION  Mouse Ig rearranged kappa-chain mRNA, clone AN12K.
ACCESSION   M19914 J03832
KEYWORDS    constant region; immunoglobulin light chain; immunoglobulin-kappa;
            processed gene.
SOURCE      Mouse (BALB/c) mature B cell, cDNA to mRNA, clone AN12K.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Rule,G.S.
  JOURNAL   Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305.
  STANDARD  full automatic
REFERENCE   2  (bases 1 to 456)
  AUTHORS   Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
  TITLE     Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-bodies
            for NMR studies
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
  STANDARD  full automatic
COMMENT     Draft entry and computer-readable sequence [2] kindly submitted by
            G.Rule, 20-JUL-1988.
FEATURES             Location/Qualifiers
     sig_peptide     19..90
                     /codon_start=1
                     /note="Ig kappa-chain signal peptide"
     mat_peptide     91..456
                     /partial
                     /codon_start=1
                     /note="Ig kappa-chain"
     CDS             19..455
                     /partial
                     /partial
                     /note="Ig kappa-chain precursor"
                     /codon_start=1
                     /translation="MGIKMESQIQVFVFVFLWLSGVDGDIVMTQSHKFMSTSVGDRVS
                     ITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPDRFTGSGSGTDFTFTISSV
                     QAEDLAVYYCHQHYSSPYTFGGGTKLEIKRADAAPTVSIFPPSX"
BASE COUNT      118 a    114 c    108 g    116 t
ORIGIN
```

```
Initial Score    =    272  Optimized Score  =    275  Significance = 21.58
Residue Identity =    86%  Matches          =    276  Mismatches   =    42
Gaps             =      1  Conservative Substitutions               =     0
```

```
                                                  X        10        20
                                                  AG-TATTGTGATGACCCAGACT
                                                  ||  ||||||||||||||| ||
   CAGATTCAGGTCTTTGTATTCGTGTTTCTCTGGTTGTCTGGTGTTGACGGAGACATTGTGATGACCCAGTCT
  40        50        60        70        80        90       100       110

         30        40        50        60        70        80        90
   CCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAAT
   | ||||||| ||      ||||  |||||||||||| | ||| ||||||||||||||||||  ||||| || |
   CACAAATTCATGTCCACATCAGTAGGAGACAGGGTCAGCATCACCTGCAAGGCCAGTCAGGATGTGAGTACT
        120       130       140       150       160       170       180

      100       110       120       130       140       150       160
   GATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTAC
   | |||||| ||||| ||||| || ||||| || |||||||||||| ||||| || |  |||||| | || |||
   GCTGTAGCCTGGTATCAACAAAAACCAGGACAATCTCCTAAACTACTGATTTACTCGGCATCCTACCGGTAC
      190       200       210       220       230       240       250
```

```
    170       180       190       200       210       220       230
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAG
|||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
ACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACGGATTTCACTTTCACCATCAGCAGTGTGCAG
  260       270       280       290       300       310       320

240       250       260       270       280       290       300
GCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAG
|||||||||||||||||||||| |||||| ||  ||||||| ||||||||||||||||||||||||||||||
GCTGAAGACCTGGCAGTTTATTACTGTCATCAACATTATAGTTCTCCGTACACGTTCGGAGGGGGGACCAAG
330       340       350       360       370       380       390

310       X
  CTGGAGATC
  ||||| ||
  CTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGT
400       410       420       430       440       450
```

13. US-07-977-702-2 (1-318)
    MMNPCRLB1   M.musculus NPCRLB1 mRNA for immunoglobulin light c

```
 ID   MMNPCRLB1  standard; RNA; ROD; 321 BP.
 XX
 AC   X70095; X51612;
 XX
 DT   19-MAR-1993 (Rel. 35, Created)
 DT   19-MAR-1993 (Rel. 35, Last updated, Version 1)
 XX
 DE   M.musculus NPCRLB1 mRNA for immunoglobulin light chain, variable
 DE   region
 XX
 KW   immunoglobulin light chain variable region.
 XX
 OS   Mus musculus (mouse)
 OC   Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
 OC   Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
 XX
 RN   [1]
 RP   1-321
 RA   Izui S.;
 RT   ;
 RL   Submitted (05-FEB-1993) on tape to the EMBL Data Library by:
 RL   S. Izui, Dept. of Pathology, Centre Medical Universitaire, 1, Rue
 RL   Michel Servet, CH-1211, geneva 4, SWITZERLAND
 XX
 CC   *source: strain=C57BL/6;
 CC   *source: tissue=lymphoid;
 CC   *source: cell_type=hybridoma;
 CC   *source: cell_line=CB1;
 CC   *source: is_germline=N;
 XX
 FH   Key             Location/Qualifiers
 FH
 FT   CDS             <1..>321
 FT                   /codon_start=1
 FT                   /product="immunoglobulin light chain, variable region"
 XX
 SQ   Sequence 321 BP; 87 A; 81 C; 77 G; 76 T; 0 other;

Initial Score    =    271  Optimized Score  =    273  Significance = 21.50
Residue Identity =    85%  Matches          =    273  Mismatches   =    45
Gaps             =      0  Conservative Substitutions              =     0

    X       10        20        30        40        50        60        70
    AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAG
```

```
   GACATTGTGATGACCCAGTCTCACAAATTCATGTCCACATCAGTTGGAGACAGGGTCAGCATCACCTGCAAG
   X       10        20        30        40        50        60        70

         80        90       100       110       120       130       140
   GCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATA
   |||||||||  ||||| || || |||||| ||||| |||||||| ||||| || ||||||||||| |||||
   GCCAGTCAGGATGTGAGTACTGCTGTAGCCTGGTATCAACAGAAACCAGGACAATCTCCTAAACTACTGATT
         80        90       100       110       120       130       140

      150       160       170       180       190       200       210
   TATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACT
   || |  |||||| | || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
   TACTCGGCATCCTACCGGTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACGGATTTCACT
      150       160       170       180       190       200       210

    220       230       240       250       260       270       280
   TTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTAC
   |||||||||||| |||||||| |||||||||||||||||||||| ||||||||  |||||||  ||||||||
   TTCACCATCAGCAGTGTGCAGCCTGAAGACCTGGCAGTTTATTACTGTCAGCAACATTATAGTACTCCGTAC
    220       230       240       250       260       270       280

  290       300       310       X
   ACGTTCGGAGGGGGGACCAAGCTGGAGATC
   |||||||||||||||||||||||||| ||
   ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAA
  290       300       310       320
```

14. US-07-977-702-2 (1-318)
    MUSIGKVN Mouse Ig germline kappa-chain V-region gene V-Ser.

```
LOCUS       MUSIGKVN     2002 bp ds-DNA             ROD       30-JUN-1987
DEFINITION  Mouse Ig germline kappa-chain V-region gene V-Ser.
ACCESSION   M14361
KEYWORDS    constant region; germline; immunoglobulin-kappa; variable region.
SOURCE      Mouse (C.C58) liver DNA, clones EMC58-[5,7,10].
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 2002)
  AUTHORS   Boyd,R.T., Goldrick,M.M. and Gottlieb,P.D.
  TITLE     Structural differences in a single gene encoding the V-k-Ser group
            of light chains explain the existence of two mouse light-chain
            genetic markers
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138 (1986)
  STANDARD  full automatic
FEATURES             Location/Qualifiers
     exon            <1071..1119
                     /number=1
                     /note="Ig kappa-chain precursor V-Ser"
     sig_peptide     join(1071..1119,1335..1346)
                     /codon_start=1
                     /note="Ig kappa-chain signal peptide"
     sig_peptide     1071..1119
                     /codon_start=1
                     /note="Ig kappa-chain signal peptide"
     intron          1120..1334
                     /note="IgK intron A"
     exon            1335..>1630
                     /number=2
                     /note="Ig kappa-chain precursor V-Ser"
     sig_peptide     1335..1346
                     /codon_start=1
                     /note="Ig kappa-chain signal peptide"
     mat_peptide     1347..1630
```

```
                    /partial
                    /codon_start=1
                    /note="Ig kappa-chain"
     iDNA           1631..>2002
                    /note="V-J intervening DNA (5' end +/- 1 bp)"
     CDS            join(1071..1119,1335..1629)
                    /partial
                    /partial
                    /note="Ig kappa-chain precursor V-Ser"
                    /codon_start=1
                    /translation="MKSQTQVFIFLLLCVSGAHGSIVMTQTPKFLPVSAGDRVTMTCK
                    ASQSVGNNVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGSGTDFTFTISSVQVED
                    LAVYFCQQHYSSP"
BASE COUNT      533 a    421 c    376 g    672 t
ORIGIN      1 bp upstream of EcoRI site; chromosome 6.

Initial Score    =    270  Optimized Score  =    284  Significance = 21.41
Residue Identity =    88%  Matches          =    291  Mismatches   =    27
Gaps             =      9  Conservative Substitutions               =     0

                                                  X       10        20
                                                  AGTATTGTGATGACCCAGACTC
                                                  ||||||||||||||||||||||
   GTGTAAATGTGTATCCTCATTATTTATCTCTGATTGCAGGTGCTCATGGGAGTATTGTGATGACCCAGACTC
    1300      1310      1320      1330      1340      1350      1360

         30        40        50        60        70        80        90
   CCAAATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATG
   |||||||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||  ||||
   CCAAATTCCTGCCTGTATCAGCAGGAGACAGGGTTACCATGACCTGCAAGGCCAGTCAGAGTGTGGGTAATA
  1370      1380      1390      1400      1410      1420      1430

      100       110       120       130       140       150       160
   ATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATATATTATGCATCCAATCGCTACA
   ||||||| |||||||||||||||||||| |||||||||||||||||||||| ||||||||||||||||||
   ATGTAGCCTGGTACCAACAGAAGCCAGGACAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACA
1440      1450      1460      1470      1480      1490      1500      1510

    170       180       190       200       210       220       230
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGG
   |||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||| ||||||||
   CTGGAGTCCCTGATCGCTTCACTGGCAGTGGATCTGGGACAGATTTCACTTTCACCATCAGCAGTGTGCAGG
        1520      1530      1540      1550      1560      1570      1580

  240       250       260       270       280       290          300
   CTGAAGACCTGGCAGTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACAC-GTTC-GGAG-GGGGGAC-C
    |||||||||||||||||||||||||||||| ||||||||||||   ||| || |   ||      || |
   TTGAAGACCTGGCAGTTTATTTCTGTCAGCAGCATTATAGCTCTCCTCCCACAGTGCTTCAGCCTCCTACAC
      1590      1600      1610      1620      1630      1640      1650

         310       X
   AA----GCTGGAGA-TC
   ||     || |||| ||
   AAACCTCCTTGAGAGTCTCACAGCTGCCTGTCCTACATACAGCTGTGGCCTTGCACACTTCCCCCTC
    1660      1670 X    1680      1690      1700      1710      1720


15. US-07-977-702-2 (1-318)
    MUSIGKCKP    Mouse Ig kappa-chain mRNA V-region (VJ), from hybr

 LOCUS       MUSIGKCKP     341 bp ss-mRNA            ROD       15-MAR-1989
 DEFINITION  Mouse Ig kappa-chain mRNA V-region (VJ), from hybridoma
             A003-40/5G7k.
 ACCESSION   M17161 J02815
 KEYWORDS    immunoglobulin light chain; immunoglobulin-kappa; joining region;
             variable region.
```

```
SOURCE      Mouse (BALB/C) anti-Blood group A hybridoma, cDNA to mRNA, clone
            A003-40/5G7k.
  ORGANISM  Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1  (bases 1 to 341)
  AUTHORS   Chen,H.-T., Kabat,E.A., Lundblad,A. and Ratcliffe,R.M.
  TITLE     Nucleotide and translated amino acid sequences of cDNA coding for
            the variable regions of the light and heavy chains of mouse
            hybridoma antibodies to blood group A and B substances
  JOURNAL   J. Biol. Chem. 262, 13579-13583 (1987)
  STANDARD  full automatic
COMMENT     Draft entry and printed copy of sequence for [1] kindly provided by
            E.A.Kabat, 04-AUG-1987.
FEATURES             Location/Qualifiers
     sig_peptide     <1..17
                     /codon_start=3
                     /note="Ig kappa-chain signal peptide"
     mat_peptide     18..>341
                     /codon_start=1
                     /note="Ig kappa-chain"
     misc_recomb     302..303
                     /note="V-region end/J-region start"
     CDS             <1..>341
                     /note="Ig kappa-chain precursor V-region;  (VJ)"
                     /codon_start=3
                     /translation="AGVDGDIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQK
                     PGQSPKLLIYSASYRYTGVPDRFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPT
                     FGGGTKLEIKR"
BASE COUNT       88 a     84 c     88 g     81 t
ORIGIN      Chromosome 6.
```

```
Initial Score    =    269  Optimized Score  =    272  Significance = 21.32
Residue Identity =    85%  Matches          =    273  Mismatches   =    45
Gaps             =      1  Conservative Substitutions              =     0
```

```
                  X        10        20        30        40        50
                  AG-TATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTTTCAGCAGGAGACAGGG
                  ||  ||||||||||||||| ||| ||||||| ||      |||| ||||||||||||
   TTGCAGGTGTTGACGGAGACATTGTGATGACCCAGTCTCACAAATTCATGTCCACATCAGTAGGAGACAGGG
           10      X 20        30        40        50        60        70

      60        70        80        90       100       110       120
   TTACCATAACCTGCAAGGCCAGTCAGAGTGTGACTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGT
   | | ||| ||||||||||||||||||  ||||| || |  ||| || ||||| || ||||| |||||||| |
   TCAGCATCACCTGCAAGGCCAGTCAGGATGTGAGTACTACTGTGGCCTGGTATCAGCAGAAACCAGGGCAAT
         80        90       100       110       120       130       140

  130       140       150       160       170       180       190
   CTCCTAAACTGCTGATATATTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGAT
   |||||||||| ||||| ||||  |||||| | || ||||||||||||||||||||||||||||||||||||
   CTCCTAAACTACTGATTTATTCGGCATCCTACCGGTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGAT
      150       160       170       180       190       200       210

 200       210       220       230       240       250       260       270
   ATGGGACGGATTTCACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAGCAGG
    |||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||||
   CTGGGACGGATTTCACTTTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAAC
    220       230       240       250       260       270       280

         280       290       300       310       X
   ATTATAGCTCTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAGATC
   |||||||  ||||   |||||||||||||||||||||||||| ||
   ATTATAGTACTCCTCCCACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGG
  290       300       310       320       330     X  340
```